

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2004, 14:44:07 ; Search time 6771 Seconds  
(without alignments)  
12137.162 Million cell updates/sec

Title: US-10-624-932-1  
Perfect score: 2752  
Sequence: 1 ccgcggggcccccgcgcccg.....tgagtgcctgaggccgccag 2752

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%		Query				Description
			No.	Score	Match	Length DB ID	
			1	960.2	34.9	2802 29	AY406491 Homo sapi
			2	950.4	34.5	2791 29	AY406493 Mus muscu
			3	923.4	33.6	3790 11	AK031655 Mus muscu
			4	872.4	31.7	3866 11	AK018177 Mus muscu
			5	814	29.6	2802 29	AY406492 Pan trogl
			6	810.4	29.4	2532 29	AY411747 Homo sapi
			7	780.4	28.4	2532 29	AY411749 Mus muscu
			8	768.6	27.9	1034 12	BI758231 603029876
			9	736.6	26.8	1532 11	BC033727 Homo sapi
			10	735.2	26.7	788 9	AI951556 wv36f04.x
c			11	722.8	26.3	843 13	BX348193 BX348193
			12	716.4	26.0	818 12	BI818609 603033362
			13	692	25.1	909 13	BX364574 BX364574
			14	678.2	24.6	2532 29	AY411748 Pan trogl
			15	672.6	24.4	934 10	BF311804 601897316
			16	666	24.2	939 13	BX345406 BX345406
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			18	645.2	23.4	1040 13	BX345407 BX345407
			19	631.2	22.9	1201 13	BX422753 BX422753
			20	618.8	22.5	756 13	BU612387 UI-M-EW0-
			21	613.2	22.3	874 13	BQ689148 AGENCOURT
			22	610.2	22.2	2775 29	AY401471 Mus muscu
			23	607	22.1	889 13	BQ691915 AGENCOURT
			24	599	21.8	2775 29	AY401469 Homo sapi
			25	596.4	21.7	662 9	AL516580 AL516580
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## ALIGNMENTS

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 genomic survey sequence.  
 ACCESSION AY406491  
 VERSION AY406491.1 GI:39762465  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2802)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 2802)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 gene <1..>2802  
 /gene="UNC5C"  
 /locus\_tag="HCM2575"

## ORIGIN

Query Match 34.9%; Score 960.2; DB 29; Length 2802;  
 Best Local Similarity 61.3%; Pred. No. 1.2e-153;  
 Matches 1682; Conservative 0; Mismatches 995; Indels 69; Gaps 6;

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Qy      57  GCCCCGCCCTGTGGCCAGCGCTCCTGGGCGATAGTCCCTCGCCGCTTGGCTCCGCGGCTCGGG 116
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Db      66  GCTCGTGCTACCTGCCCTGGCCCTGCTCAGCGCCAGCGGCACTGGCTCCGCCGCCCAAGA 125

Qy      117 TGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
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Db      126 TGATGACTTTTTTCATGAACTCCAGAACTTTTCTTCTGATCCACCTGAGCCTCTGCC 185

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Qy 177 CCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGT 236  
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Qy 237 GTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCA 296  
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 Db 246 CTGTAAAGCAAGCCCTGCCACCCAGATCTATTTCAAGTGTAATAGTGAATGGGTTCATCA 305

Qy 297 GGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGT 356  
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 Db 306 GAAGGACCACATAGTAGATGAAAGAGTAGATGAAACTTCCGGTCTCATTTGTCCGGGAAGT 365

Qy 357 CCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTGCGGCTGGAGGAATACTGGTG 416  
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 Db 366 GAGCATTGAGATTTTCGCGCCAGCAAGTGAAGAAGTCTTTGGACCTGAAGATTACTGGTG 425

Qy 417 CCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCCTACATCCGCAT 476  
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Qy 477 AGC-----CAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCT 530  
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 Db 486 TGCATNNNNNNNNNNNCGGAAGACATTTGAGCAGGAACCCCTAGGAAAGGAAGTGTCTTT 545

Qy 531 GGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGGCATCCCTCCAGCCGAGGTGGA 590  
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Qy 591 GTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCG 650  
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Qy 651 GGAGCACAGCCTGGTGGTGCACAGGCCCCGCCTTGCTGACACGGCCAACCTACACCTGCGT 710  
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Qy 831 GCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGA 890  
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Qy 891 GGGGCAGAATGTCCAGAAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAG 950  
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Qy 951 CCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTG 1010  
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Qy 1071 CAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTA 1130  
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 Db 1086 GAACTGCACTGATGGGCTTTGCATGCAGACTGCTCCTGATTGAGATGATGTGCTCTCTA 1145

Qy 1131 TGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCT 1187  
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Qy 1308 CATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCA 1367  
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Qy 1368 GGATG-----GGCCCAGCCCCAAGTTCCAGCTCACCAAT-----GGGCACCTGCTCAGCCC 1418  
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Qy 1479 CGTCTCCCGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACAT 1538  
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 Db 1497 TACGTCCAAGCTGTCCCCTCAGATGACCCAGTCGTTGTTGGAGAATGAAGCCCTCAGCCT 1556

Qy 1539 GA-----CCTATGGGACCTTCAA 1556  
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Qy	1917	CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	1976
Db	1977	CCACATCCTCACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGC	2036
Qy	1977	TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	2036
Db	2037	GGCTGCGAAGCGCCTCAAGCTGGCCATCTTTGGGCCCTGTGCTGCTCCTCGCTGGAGTA	2096
Qy	2037	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	2096
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Qy	2157	TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT	2216
Db	2217	CACCCACAACCTGCGCCTGTCAATTACGATATCGCCATTCCCTCTGGAAGAGCAAATT	2276
Qy	2217	CCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	2276
Db	2277	GCTGGCTAAATATCAGGAAATTCCATTTTACCATGTTTGGAGTGGATCTCAAAGAAACCT	2336
Qy	2277	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	2336
Db	2337	GCACTGCACCTTCACTCTGGAAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAAC	2396
Qy	2337	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	2396
Db	2397	CTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAGCTCAACTGCACCGTGTGAGA	2456
Qy	2397	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGT	2456
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Qy	2457	GGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	2516
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Db	2577	TGCCCCCAGACGAGAGGCCATGACTGGAGGATGCTGGCCCATAAGCTGAACCTGGACAG	2636
Qy	2577	CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA	2636
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Qy 2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742

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# RESULT 2

AY406493

LOCUS AY406493 2791 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406493

VERSION AY406493.1 GI:39762467

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2791)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2791)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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## ORIGIN

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Best Local Similarity 62.3%; Pred. No. 5.6e-152;  
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Db 158 TTCCATCTGACCCACCTGAGCCATTGCCACACTTCCTCATTGAGCCCGAGGAAGCTTACA 217

Qy 209 TCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCT 268

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Qy	329	GGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGA	388
Db	338	AAACCTCTGGTCTAATTGTGAGAGAAGTGAGCATTGAGATTTACGCCAGCAGGTGGAGG	397
Qy	389	AGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCA	448
Db	398	AACTGTTTGGGCCTGAAGATTACTGGTGCCAGTGTGTGGCCTGGAGCTCAGCAGGCCTA	457
Qy	449	CCAAGAGTCAGAAGGCCCTACATCCGCATAGCCAG-----ATTGCGCAAGAACTTCGAGC	502
Db	458	CGAAGAGTCGGAAGGCATACGTGCGCATTGCGTTTCCAGATCTGCGGAAGACATTCGAGC	517
Qy	503	AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC	562
Db	518	AGGAACCCCTTGGGAAAGGAAGTGTCTTGGAGCAGGAAGTCTTACTCCAGTGTGCGCCAC	577
Qy	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCCGT	622
Db	578	CTGAAGGGATCC-----GTAGAATGGCTAAAGAATGAAGACATAATTGATCCTG	626
Qy	623	CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCC	682
Db	627	CTGAAGATCGGAACCTTTTATATTACTATCGATCACAACTGATCATCAAGCAAGCCCGAC	686
Qy	683	TTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGACG	742
Db	687	TCTCAGATACAGCAAATTATACCTGTGTTGCCAAAAATATTGTTGCCAAGAGAAAAAGCA	746
Qy	743	CCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG	802
Db	747	CCACAGCCACTGTTCATCGTGTATGTTAATGGTGGCTGGTCCACCTGGACAGAGTGGTCTG	806
Qy	803	TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG	862
Db	807	TGTGTAACAGCCGCTGTGGGCGAGGATATCAGAAACGCACAAGAACCTGCACCAACCCAG	866
Qy	863	CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCA	922
Db	867	CCCCACTCAATGGTGGGGCCTTCTGTGAGGGGCGAGTGTGCAGAAAATAGCATGCACTA	926
Qy	923	CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCCTGGAGCAAGTGGTTCGGCCTGTGGGCTGG	982
Db	927	CGTTATGTCCAGTGGATGGTAGGTGGACTTCATGGAGCAAATGGTCAACCTGTGGGACTG	986
Qy	983	ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG	1042
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Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGG---CCTCATCGCCGTGGCCGTCTGCC 1159  
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Qy 1220 CAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
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Qy 1280 GCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCA 1339  
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Db 1283 -----GCTGCCAGACAAGATCTCCTGGCTGTCCCCCTGACCTCACCTCAGCTGCAGCCA 1337

Qy 1340 CCTACCAGGGCAGTCTCTGTCCCCGGCAGGATG-----GGCCCAGCCCCAAGTTCCAGCT 1394  
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Db 1338 TGTACAGGGGACCTGTCTATGCTCTGCATGATGTCTCAGACAAAATCCCAATGACCAACT 1397

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Qy 1455 TCCCACCTC----TGAGGCCGAGGAGTTCGTCTCCCGCTCTCCACCC----- 1498  
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Db 1518 CCTTGCTAGAGAATGAGGCCCTTAACCTGAAGAACCAGAGCCTCGCAAGACAGACTGACC 1577

Qy 1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588  
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Db 1578 CATCCTGCACAGCATTTGGTACCTTCAACTCTCTTGGGGGTACCTCATCATTCTTAATT 1637

Qy 1589 CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT 1648  
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Db 1638 CAGGAGTAAGCTTGCTGATTCCCCTGCGGGCCATTCTCAGGGGAGAGTCTATGAAATGT 1697

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Db 1758 TTACCCCTGTGGTGAGCTGTGGGCCTCCTGGAGCTCTGCTGACCCGCCCTGTCATCCTCA 1817

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 Db 2358 TAAACACAGTGGAAGTGGTTTGCAAACCTCTGTGTGCGGCAGGTTGAAGGAGAAGGGCAGA 2417

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 Db 2418 TCTTCCAGCTCAACTGTACTGTGTGTCAGAGGAACCTACTGGCATCGACTTACCTCTCCTGG 2477

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QY 2729 AGGCTGAGTGCTGA 2742  
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Db 2778 AAGGACAGTATTGA 2791

RESULT 3

AK031655

LOCUS AK031655 3790 bp mRNA linear HTC 18-SEP-2003

DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

ACCESSION AK031655

VERSION AK031655.1 GI:26327502

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

(bases 1 to 3790)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source Location/Qualifiers

1. .3790

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM\_DB:6030473H24"

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/clone="6030473H24"

/sex="male"

/tissue\_type="testis"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="13 days embryo"

CDS 118. .2970

/note="unnamed protein product; putative unc5 homolog (C. elegans) 3 (MGD|MGI:1095412, GB|NM\_009472, evidence: BLASTN, 99%, match=464)"

/codon\_start=1

/protein\_id="BAC27495.1"

/db\_xref="GI:26327503"

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ORIGIN

Query Match 33.6%; Score 923.4; DB 11; Length 3790;  
Best Local Similarity 61.3%; Pred. No. 2.7e-147;  
Matches 1659; Conservative 0; Mismatches 926; Indels 120; Gaps 6;

Qy	149	TGCCTGGTGCCAAACCCGGACCTGCTTCCCCACTTCCTGGTGAGCCCCGAGGATGTGTACA	208
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Qy	449	CCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGC	508
Db	575	CGAAGAGTCGGAAGGCATACGTGCGCATTGCGTATCTGCGGAAGACATTCGAGCAGGAAC	634
Qy	509	CGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGG	568
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Qy	569	GCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGG	628
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Qy      2438 CGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGA 2497
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Db      2666 GTACCATCACCCTGTCTACCGGACCAAGTGCTTTCAGCATTCCTCTCCCTATCCGGCAGA 2725
Qy      2498 AGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCC 2557
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Db      2726 AGCTATGCAGCAGCCTGGATGCCCTCAAACAAGAGGCCATGACTGGAGGATGCTGGCCC 2785
Qy      2558 AGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCA 2617
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Db      2786 ATAAACTCAACCTGGACAGGTACTTGAATTACTTTGCCACCAAATCGAGCCCAACTGGCG 2845
Qy      2618 TGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTG 2677
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Db      2846 TAATCCTGGATCTTTGGGAAGCACAGAACTTCCAGATGGAAACCTGAGCATGCTGGCAG 2905
Qy      2678 CAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGT 2737
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Db      2906 CCGTCCTGGAAGAAATGGGAAGACATGAGACAGTGGTGTACTTGGCAGCAGAAGGACAGT 2965
Qy      2738 GCTGA 2742
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Db      2966 ATTGA 2970

```

#### RESULT 4

AK018177

LOCUS AK018177 3866 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330415E02 product:TRANSMEMBRANE RECEPTOR UNC5H2 homolog [Rattus norvegicus], full insert sequence.

ACCESSION AK018177

VERSION AK018177.1 GI:12857775

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

#### REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

#### REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3866)

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved

with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

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                        /db_xref="MGI:1910526"
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                        /dev_stage="adult"
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                        /db_xref="GI:12857776"
                        /translation="MRARSGVRSALLLALLLCWDPTPSLAGVDSAGQVLPDSYPSAPA
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                        AKEVPLDHEVLLQCRPPEGVPVAEVEWLKNEVDVIDPAQDTNFLTIDHNLIIIRQARLS
                        DTANYTCVAKNIVAKRRSTAATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNP
                        APLNGGAFCEGQAFQKTACTTVCPVDGAWTEWSKWSACSTECAHWRSRECMAPPQNG
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                        AEGVIVYRRNCRDFDITDSSAALTGGFHPVNFKTARPNNPQLLHPSAPPDLTASAG
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                        MGESYSRSAVKRLQLAIFAPALCTSLEYSRLVYCLEDTPVALKEVLELERTLGGYLVE
                        EPKPLLFKDSYHNLRLSLHDI PHAHWRSKLLAKYQEIPFYHVWNGSQRALHCTFTLER
                        HSLASTEFTCKVCVRQVEGEGQIFQLHTTIAETPAGSLDALCSAPGNAITTQLGPYAF
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#### ORIGIN

Query Match 31.7%; Score 872.4; DB 11; Length 3866;  
Best Local Similarity 60.6%; Pred. No. 1.4e-138;  
Matches 1646; Conservative 0; Mismatches 941; Indels 129; Gaps 8;

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Db      600  AACAAAGCCAGTGGAAGTGCAGTGCAGAGCCTTCCCTGCCACGCAGATCTACTTCAAGTGT 659

Qy      277  AACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGT 336
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Db	660	AATGGCGAGTGGGTGAGCCAGAAATGACACAGTACACAGGAGAGCCTGGATGAGGCCACA	719
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Qy	397	GGGCTGGAGGAATACTGGTGCCAGTGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGT	456
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Qy	577	CCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAAT	636
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Qy	757	ATCGTCTACGTGAACGGTGGGTGGTGCAGTGGACCGAGTGGTCCGTCTGCAGCGCCAGC	816
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Qy	817	TGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGG	876
Db	1200	TGTGGCCGAGGCTGGCAGAAGCGTACTCGGACCTGCACCAATCCAGCCCCACTCAATGGA	1259
Qy	877	GGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTA	936
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Qy	937	GACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCTGTGGGCTGGACTGCACCCACTGG	996
Db	1320	GATGGAGCGTGGACCGAGTGGAGCAAGTGGTCTGCCTGCAGCACAGAGTGTGCGCACTGG	1379
Qy	997	CGGAGCCGTGAGTGCTCTGACCCAGCACCCTCGCAACGGAGGGGAGGAGTGCCAGGGCACT	1056
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Qy	1057	GACCTGGACACCCGCAACTGTACAGTGACCTCTGTGTACACAGTGCTTCTGGCC-----	1111
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Qy	1112	-----CTGAGGACGTGGCCCTCTATGTGGGCTCATC	1143
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Qy	1144	GCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTC---CTCATCCTCGTTTATTGCCGG	1200
Db	1560	GTGGCCGTCTTTGTGGTGGTAGCGGTTCTCATGGCCGAGGGAGTGATCGTATACCGGAGA	1619
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGT---CCATTCTCACCTCAGGCTTC	1257
Db	1620	AACTGCCGGGACTTCGACACGGACATCACCGACTCCTCTGCGGCCCTCACTGGTGGCTTC	1679
Qy	1258	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCT-----CACCATC	1311
Db	1680	CACCCTGTCAACTTCAAGACTGCAAGGCCCAACAACCCGCAGCTCCTGCACCCGTCCGCC	1739
Qy	1312	CAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA-	1370
Db	1740	CCTCCAGACCTAACGGCCAGTGCTGGCATCTACCGCGGGCCTGTGTATGCCCTGCAGGAC	1799
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Db	1860	ATCAAGGTCTATAACTCCAGCACCATCGGTTCTGGGTCTGGCCTGGCTGATGGAGCCGAC	1919
Qy	1417	CCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAG	1476
Db	1920	CTGCTGGGTGTCTCTCCCGCCGGGCACGTACCCAGGCGATTCTCCCGGGACACCCATTTC	1979
Qy	1477	TTCGTCTCCCGCCTCTCCACCC-----AGAACTACTTCGCTCCCTGCCCCGAGGCACC	1530
Db	1980	CTGCACCTGCGCAGTGCCAGCCTTGGTTCCAGCACCTCCTGGGCCTACCTCGGGACCCC	2039
Qy	1531	AGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACA	1590
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Qy	1591	GGTATCAGCCTCCTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTAC	1650
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Qy	1651	CTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTG	1710
Db	2160	CTACATATCAACAAGGCCGAAAGCACCCCTCCCACTTTCAGAAGGTTCCAGACAGTATTG	2219
Qy	1711	AGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCT	1770
Db	2220	AGCCCCTCGGTGACCTGTGGGCCCACAGGCCTACTCCTGTGCCGCCCTGTCGTCTCTCACC	2279
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Db	2280	GTGCCCCACTGTGCTGAAGTCATCGCTGGAGACTGGATCTTTCAGCTCAAGACCCAGGCC	2339
Qy	1831	TGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTAC	1890
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 Db 2520 CCAGCCCTCTGCACCTCCCTGGAGTATAGCCTCAGGGTCTACTGTCTGGAGGACACACCT 2579

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 Db 2760 GTCTGGAATGGCAGCCAGAGAGCCCTGCACTGCACTTTACCCTGGAGAGGCATAGCCTG 2819

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Qy 2371 TTCAGCATCAACTTCAACATCACC---AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTG 2427  
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Qy 2728 GAGGCTGAGTGCTGAG 2743

Db                    3240    || |    || |||||    3255  
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## RESULT 5

AY406492

LOCUS	AY406492	2802 bp	DNA	linear	GSS 15-DEC-2003
-------	----------	---------	-----	--------	-----------------

DEFINITION Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406492

VERSION AY406492.1 GI:39762466

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2802)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT      This sequence was made by sequencing genomic exons and ordering  
                 them based on alignment.

FEATURES	Location/Qualifiers
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## ORIGIN

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Matches 1477; Conservative 0; Mismatches 1200; Indels 69; Gaps 6;

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nb 66 GCTCGTGCTACCTGCCCTGGCCCTGCTCAGCGCCAGCGGCACTGGCTCCGCCGCCCAAGA 125

QY 117 TGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176

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Qy	237	GTGCAAGGCC-----GTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGT	290
Db	246	CTGTAAAGCAAGCCCTGNN	305
Qy	291	GCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCAT	350
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Qy	351	GGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAGGAATA	410
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Qy	411	CTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACAT	470
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Qy	471	CCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCT	530
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Qy	531	GGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGA	590
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Qy	591	GTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCG	650
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Qy	651	GGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT	710
Db	666	TGATCACAACTCATCATAAAGCAGGCCCGACTCTCTGATACTGCAAATTATACCTGTGT	725
Qy	711	GGCCAAGAACATCGTGGCACGTCGCCGACGCGCCTCCGCTGCTGTCATCGTCTACGTGAA	770
Db	726	TGCCAAAAACATTTGTTGCCAAGAGGAAAAAGTACAACTGCCACTGTCATAGTCTATGTCAA	785
Qy	771	CGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGCTCTGCACGCCAGCTGTGGGCGCGGCTG	830
Db	786	CGGTGGCTGGTCCACCTGGACGGAGTGGTCTGTGTGTAACAGCCGCTGTGGACGAGGGTA	845
Qy	831	GCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGA	890
Db	846	TCAGAAACGTACAAGGACTTGTACCAACCCGGCACCCTCAATGGGGGTGCCTTCTGTGA	905
Qy	891	GGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAG	950
Db	906	AGGGCAGAGTGTGCAGAAAATAGCCTGTACTACGTTATGCCAGTGGAATGGCAGGTGGAC	965
Qy	951	CCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTG	1010
Db	966	GCCATGGAGCAAGTGGTCTACTTGTGGAACAGTGTGACCCACTGGCGCAGGAGGGAGTG	1025
Qy	1011	CTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCG	1070

Db	1026	<div> <div>   </div> CACGGCGCCAGCCCCCAAGAATGGAGGCAAGGACTGCGATGGCCTCGTCTTGCAATCCAA </div>	1085
Qy	1071	CAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTA	1130
Db	1086	<div> <div>   </div> GAAGTGCAGTATGATGGGCTTTGCATGCAGACTGCTCCTGATTGATGATGTTGCTCTCTA </div>	1145
Qy	1131	TGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCT	1187
Db	1146	<div> <div>   </div> TGTTGGGATTGTGATAGCAGTGATCGTTTGCCTGGCGATCTCTGTAGTTGTGGCCTTGTT </div>	1205
Qy	1188	CGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCAC	1247
Db	1206	<div> <div>   </div> TGTGTATCGGAAGAATCATCGTGACTTTGAGTCAGATATTATTGACTCTTCGGCACTCAA </div>	1265
Qy	1248	CTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCAC	1307
Db	1266	<div> <div>   </div> TGGGGGCTTTCAGCCTGTGAACATCAAG-----GCAGCAAGACAAGATCTGCTGGC </div>	1316
Qy	1308	CATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCA	1367
Db	1317	<div> <div>   </div> TGTACCCCCAGACCTCACGTGAGTGCAGCCATGTACAGAGGACCTGTCTATGCCCTGCA </div>	1376
Qy	1368	GGATG-----GGCCCAGCCCCAAGTTCCAGCTCACCAAT----GGGCACCTGCTCAGCCC	1418
Db	1377	<div> <div>   </div> TGACGTCTCAGACAAAATCCCAATGACCAACTCTCCAATTCTGGATCCACTGCCCAACCT </div>	1436
Qy	1419	CCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTT	1478
Db	1437	<div> <div>   </div> GAAAATCAAAGTGTACAACACCTCAGGTGCTGTCAACCCCCAAGATGACCTCTCTGAGTT </div>	1496
Qy	1479	CGTCTCCCGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACAT	1538
Db	1497	<div> <div>   </div> TACGTCCAAGCTGTCCCCTCAGATGACCCAGTCATTGTTGGAGAATGAAGCCCTCAGCCT </div>	1556
Qy	1539	GA-----CCTATGGGACCTTCAA	1556
Db	1557	<div> <div>   </div> GAAGAACCAGAGTCTAGCAAGGCAGACTGATCCATCCTGTACCGCATTTGGCAGCTTCNN </div>	1616
Qy	1557	CTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGA	1616
Db	1617	<div> <div>   </div> NTNGCTGGGNNNCACCTTATTGTTCCCAATTGAGGAGTCAGCTTGTGATTCCCCTGG </div>	1676
Qy	1617	TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT	1676
Db	1677	<div> <div>   </div> GGCCATTCCTCAAGGGAGAGTCTACGAAATGTATGTGACTGTACACAGGAAAGAACTAT </div>	1736
Qy	1677	GAGGTTGCCCCCTAGCTGGCTGTCAGACCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC	1736
Db	1737	<div> <div>   </div> GAGGCCACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGAGCTGTGGGCCCCC </div>	1796
Qy	1737	TGGCGTCCTGCTCACCCTGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC	1796
Db	1797	<div> <div>   </div> AGGAGCTCTGCTCACCCTGGCCCGTCTGCTTACTATGCATCACTGCGCAGACCCCAATAC </div>	1856
Qy	1797	TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	1856
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Db 1857 CGAGGACTGGAAAATACTGCTCAAGAACCAGGCAGCACAGGGACAGTGGGAGGATGTGGT 1916

Qy 1857 GCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG 1916  
| | | | | | | | | | | | | | | | | | | | | |

Db 1917 GGTGGTCGGGGAGGAAAACCTTACCACCCCTGCTACATTAGCTGGATGCAGAGGCCTG 1976

Qy 1917 CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC 1976  
| | | | | | | | | | | | | | | | | | | | | |

Db 1977 CCACATCCTCACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGC 2036

Qy 1977 TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA 2036  
| | | | | | | | | | | | | | | | | | | | | |

Db 2037 GGCTGCGAAGCGCCTCAAGCTGGCCATCTTTGGGCCCTGTGCTGCTCCTCGCTGGAGTA 2096

Qy 2037 CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT 2096  
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Db 2097 CAGCATCCGAGTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAAATTTTACATCT 2156

Qy 2097 GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAG 2156  
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Db 2157 TGAGAGACAGATGGGAGGACAGCTCCTAGAAGAACCTAAGGCTCTTCATTTTAAAGGCAG 2216

Qy 2157 TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT 2216  
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Db 2217 CACCCACAACCTGCGCCTGTCAATTACGATATCGCCCATTCCTCTGGAAGAGCAAATT 2276

Qy 2217 CCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT 2276  
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Db 2277 GCTGGCTAAATATCAGNNNAACCT 2336

Qy 2277 GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT 2336  
| | | | | | | | | | | | | | | | | | | | | |

Db 2337 GCACTGCACCTTCACTCTGGAAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAAC 2396

Qy 2337 GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA 2396  
| | | | | | | | | | | | | | | | | | | | | |

Db 2397 CTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAGCTCAACTGCACCGTGTGAGA 2456

Qy 2397 GGACACAAGGTTTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT 2456  
| | | | | | | | | | | | | | | | | | | | | |

Db 2457 GGAACCTACTGGCATCGATTTGCCGCTGCTGGATCCTGCGAACACCATCACACGGTTCAC 2516

Qy 2457 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA 2516  
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Db 2517 GGGGCCAGTGCTTTCAGCATCCCTCTCCCTATCCGGCAGAAGCTCTGTAGCAGCCTGGA 2576

Qy 2517 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG 2576  
| | | | | | | | | | | | | | | | | | | | | |

Db 2577 TGCCCCCAGACGAGAGGCCATGACTGGAGGATGTGGCCCATAAGCNNNNNNNNNNNNNN 2636

Qy 2577 CCATCTCAGCTTCTTTGCCCTCCAAGCCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 2636  
| | | | | | | | | | | | | | | | | | | | | |

Db 2637 GTACTTGAATTACTTTGCCACCAAATCCAGCCCAACTGGCGTAATCCTGGATCTTTGGGA 2696

Qy 2637 GGC GCGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 2696  
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Db 2697 AGCACAGAACTCCCAGATGGAAACCTGAGCATGCTGGCAGCTGTCTTGAAGAAATGGG 2756

Qy 2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGCTGA 2742  
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 Db 2757 AAGACATGAAACGGTGGTGTCCTTAGCAGCAGAAGGGCAGTATTAA 2802

RESULT 6

AY411747

LOCUS	AY411747	2532 bp	DNA	linear	GSS	12-DEC-2003
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DEFINITION Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION      AY411747

VERSION AY411747.1 GI:39767715

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2532)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE      Inferring nonneutral evolution from human-chimp-mouse orthologous  
             gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2532)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT      This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES	Location/Qualifiers
source	1. .2532 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
gene	<1. .>2532 /locus_tag="HCM4327"

ORIGIN

Query Match 29.4%; Score 810.4; DB 29; Length 2532;  
Best Local Similarity 61.1%; Pred. No. 4.6e-128;  
Matches 1540; Conservative 0; Mismatches 851; Indels 129; Gaps 9;

QY            352 GAGGTCCGCATTAATGCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGGCTGGAGGAATAC    411  
             ||||| |     ||     || ||     ||||||||| ||| |     || ||||||||| |||

Qy 412 TGGTGCCAGTGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATC 471  
|||||

Db 73 TGGTGCCAGT GCGTGGCCTGGAGCTCCGCGGGCACCACCAAGAGTCGCCGAGCCTACGTC 132

Qy	472	CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAAGGAGGTGTCCCTG	531
Db	133	CGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTG	192
Qy	532	GAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGGCATCCCTCCAGCCGAGGTGGAG	591
Db	193	GACCATGAGGTTCTCCTGCAGTGCCGCCCCGCCGAGGGGGTGCCTGTGGCCGAGGTGGAA	252
Qy	592	TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGG	651
Db	253	TGGCTCAAGAATGAGGATGTCATCGACCCACCCAGGACACCAACTTCCTGCTCACCATC	312
Qy	652	GAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTG	711
Db	313	GACCACAACCTCATCATCCGCCAGGCCCGCCTGTCGGACACTGCCAACTATACCTGCGTG	372
Qy	712	GCCAAGAACATCGTGGCACGTCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAAC	771
Db	373	GCCAAGAACATCGTGGCCAAACGCCGAGCACCCTGCCACCGTCATCGTCTACGTGAAT	432
Qy	772	GGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCACGCGCCAGCTGTGGGCGCGGCTGG	831
Db	433	GGCGGCTGGTCCAGCTGGGCAGAGTGGTCACCCCTGCTCCAACCGCTGTGGCCGAGGCTGG	492
Qy	832	CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAG	891
Db	493	CAGAAGCGCACCCGGACCTGCACCAACCCCGCTCCACTCAACGGAGGGGCGCTTCTGCGAG	552
Qy	892	GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC	951
Db	553	GGCCAGGCATTCCAGAAGACCGCCTGCACCACCATCTGCCCAGTCGATGGGGCGTGGACG	612
Qy	952	CCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC	1011
Db	613	GAGTGGAGCAAGTGGTCAGCCTGCAGCACTGAGTGTGCCCACTGGCGTAGCCGCGAGTGC	672
Qy	1012	TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC	1071
Db	673	ATGGCGCCCCACCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTGCTCGACTCTAAG	732
Qy	1072	AACTGTACCAAGTGACCTCTGTGTACACAGTGCTTCT-----	1107
Db	733	AACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAACCTAAGCGACCCCAACAGCCAC	792
Qy	1108	-----GGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC---ATCGCCGTGGCCGTC	1155
Db	793	CTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTG	852
Qy	1156	TGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTG	1215
Db	853	GTCGTGGCAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTC	912
Qy	1216	GACTCAGATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATC	1272
Db	913	GACACAGACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTT	972

Qy	1273	AAGCCACAGCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGC	1326
Db	973		
		973 AAGACGGCAAGGCCAGCAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACA	1032
Qy	1327	ACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGG-----	1374
Db	1033		
		1033 GCCAGCGCCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATC	1092
Qy	1375	-----CCCCAGTTCAGCTCACCA--	1399
Db	1093		
		1093 CCCATGACCAACTCTCCTCTGCTGGACCCCTTACCAGCCTTAAGGTCAAGGTCTACAGC	1152
Qy	1400	-----ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCC-----ACACA	1440
Db	1153		
		1153 TCCAGCACCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTG	1212
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Db	1213		
		1213 CCGCCTGGCACATAACCCTAGCGATTCGCCCGGGACACCCACTTCCTGCACCTGCGCAGC	1272
Qy	1501	AACTACTTCCGCTC-----CCTGCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1273		
		1273 GCCAGCCTCGGTTCCCAGCAGCTCTTGGGCTGCCCGAGACCCAGGGAGCAGCGTCAGC	1332
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1333		
		1333 GGCACCTTTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTG	1392
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1393		
		1393 GTGCCCAATGGAGCCATTCCCCAGGGCAAGTTCACGAGATGTATCTACTCATCAACAAG	1452
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1453		
		1453 GCAGAAAGTACCCTCCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCCTCGGTGACC	1512
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1513		
		1513 TGTGGACCCACAGGCCTCCTGCTGTGCCGCCCGTCATCCTCACCATGCCCCACTGTGCC	1572
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1573		
		1573 GAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCCCACCAGGGCCACTGG	1632
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1633		
		1633 GAGGAGGTGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAG	1692
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1693		
		1693 CCCAGGGCCTGTACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCC	1752
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1753		
		1753 TATTCGCGCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACC	1812
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085



Db	1813		TCCCTGGAGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAG	1872
Qy	2086		GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCCTGCAC	2145
Db	1873		GTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGTTGGAGGAGCCGAAACCGCTAATG	1932
Qy	2146		TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2205
Db	1933		TTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTGG	1992
Qy	2206		AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2265
Db	1993		AGGAGCAAGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGC	2052
Qy	2266		CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2053		CAGAAGGCCCTCCACTGCACCTTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTC	2112
Qy	2326		GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2113		ACCTGCAAGATCTGCGTGCAGCAAGTGGAAGGGGAGGCCAGATATTCCAGCTGCATACC	2172
Qy	2386		AACATCACCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173		ACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCCTGGCAGCACT	2232
Qy	2443		GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2502
Db	2233		GTCACCACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATA	2292
Qy	2503		ATTTCCAGCCTGGACCCACCCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA	2562
Db	2293		TGCAACAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAG	2352
Qy	2563		CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC	2622
Db	2353		CTCTCTATGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATC	2412
Qy	2623		CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA	2682
Db	2413		CTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCC	2472
Qy	2683		GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2742
Db	2473		TTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA	2532

# RESULT 7

AY411749

LOCUS AY411749 2532 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY411749

VERSION AY411749.1 GI:39767717

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

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ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE     1   (bases 1 to 2532)
AUTHORS       Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE         Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL        Science 302 (5652), 1960-1963 (2003)
PUBMED        14671302
REFERENCE     2   (bases 1 to 2532)
AUTHORS       Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE         Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT       This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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    gene              <1..>2532
                     /locus_tag="HCM4327"
ORIGIN
Query Match           28.4%; Score 780.4; DB 29; Length 2532;
Best Local Similarity 60.1%; Pred. No. 6.3e-123;
Matches 1515; Conservative 0; Mismatches 876; Indels 129; Gaps 8;

Qy          352 GAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAGGAATAC 411
               ||||| |  || | || ||||||| || ||| | | ||||||| ||||| |||
Db          13  GAGGTGCAGATCGAGGTGTCACGGCAGCAAGTGGAGGAACTCTTCGGGCTCGAGGACTAC 72

Qy          412 TGGTGCCAGTGC GTGGCATGGAGCTCCTCGGGCACCAAGAGTCAGAAGGCCTACATC 471
               ||||||||||||||| ||||||| ||||| || ||||||| ||||| |||
Db          73  TGGTGCCAGTGC GTGGCCTGGAGCTCTTCGGGA ACTACCAAGAGTCGCCGAGCCTACATC 132

Qy          472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTG 531
               ||||| |||  ||||||||||||| || ||||||| ||||||||||||| || |||
Db          133 CGCATTGCCTACTTGCGCAAGAACTTTGACCAGGAGCCTCTGGCCAAGGAGGTACCCTTG 192

Qy          532 GAGCAGGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGGCATCCCTCCAGCCGAGGTGGAG 591
               || || |  || | |||| | |||| | ||||||| | ||| || |||||||
Db          193 GATCATGAGGTCCTTCTG CAGTGCCGCCACCGGAGGGAGTGCCTGTGGCTGAGGTGGAA 252

Qy          592 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATA CATCACGCGG 651
               ||||| ||| || || | | |||| | | |||| | || | |||||
Db          253 TGGCTCAAGAATGAAGATGTCATTGACCCGCTCAGGACACTA AACTTCCTGCTCACCATT 312

Qy          652 GAGCACAGCCTGGTGGT GCGACAGGCCCGCCTTGCTGACACGGCCA ACTACACCTGCGTG 711
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Db 313 GACCACAACCTCATCATCCGCCAGGCGCGCCTCTCAGACACGGCCAACTACACCTGTGTG 372  
 Qy 712 GCCAAGAACATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAAC 771  
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 Db 373 GCCAAGAATATCGTGGCCAAGCGCCGGAGCACCACGGCCACAGTCATCGTCTATGTGAAT 432  
 Qy 772 GGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 831  
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 Db 433 GGAGGCTGGTCCAGCTGGGCAGAGTGGTCACCCTGTTCCAATCGCTGTGGCCGAGGCTGG 492  
 Qy 832 CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAG 891  
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 Db 493 CAGAAGCGTACTCGGACCTGCACCAATCCAGCCCCACTCAATGGAGGCGCCTTCTGTGAG 552  
 Qy 892 GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC 951  
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 Db 553 GGACAGGCCTTCCAGAAGACAGCTTGCACCACCGTGTGCCCAGTGGATGGAGCGTGGACC 612  
 Qy 952 CCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC 1011  
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 Db 613 GAGTGGAGCAAGTGGTCTGCCTGCAGCACAGAGTGTGCGCACTGGCGCAGCCGCGAGTGC 672  
 Qy 1012 TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC 1071  
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 Db 673 ATGGCACCGCCACCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTACTTGACTCCAAG 732  
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 Db 733 AACTGCACTGATGGGCTGTGCGTGTGAATCAGAGAACTCTAAACGACCCTAAAAGCCAC 792  
 Qy 1120 -----GTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGC 1158  
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 Db 793 CCCCTGGAGACATCGGGAGATGTGGCACTGTACGCAGGCCTTGTGGTGGCCGTCTTTGTG 852  
 Qy 1159 CTGGTCTCTGCTGCTGTGCTTGTCT---CATCCTCGTTTATTGCCGAAGAAGGAGGGGCTG 1215  
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 Db 853 GTGGTAGCGGTTCTCATGGCCGTGGGAGTGATCGTATACCGGAGAACTGCCGGGACTTC 912  
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 Qy 1327 ACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGG----- 1373  
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 Db 1033 GCCAGTGTGGCATCTACCGCGGGCCTGTGTATGCCCTGCAGGACTCCGCCGACAAGATC 1092  
 Qy 1374 -----GCCCAGCCCCAAGTTCAGCTCACCAAT 1401  
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 Qy 1402 GGGCACCTGCTCAG-----CCCCCTGGGTGGCGGC 1431  
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 Db 1153 TCCAGCACCATCGGTTCTGGGTCTGGCCTGGCTGATGGAGCCGACCTGCTGGGTGTCCTC 1212

Qy 1432 CGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTC 1491  
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Qy 1492 TCCACCCAGAACT-----ACTTCCGCTCCCTGCCCGAGGCACCAGCAACATGACCTAT 1545  
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Qy 1546 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC 1605  
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Qy 1606 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1665  
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Qy 1666 CCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTGAGACCCTGCTGAGTCCCATCGTTAGC 1725  
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Qy 1726 TGTGGACCCCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785  
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 Db 1513 TGTGGGCCCCACAGGCCTACTCCTGTGCCGCCCTGTGCTCCTCACCGTGCCCCACTGTGCT 1572

Qy 1786 GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG 1845  
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 Db 1573 GAAGTCATCGCTGGAGACTGGATCTTTAGCTCAAGACCCAGGCCCATCAGGGCCACTGG 1632

Qy 1846 GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG 1905  
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 Db 1633 GAGGAGGTGGTGACCTTGGATGAGGAGACCCCTCAACACACCCTGCTACTGCCAGCTGGAG 1692

Qy 1906 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCC 1965  
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 Db 1693 GCTAAGTCCTGCCACATCCTGCTGGACCAGCTGGGTACCTACGTATTCATGGGCGAGTCC 1752

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Qy 2026 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2085  
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Qy 2086 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC 2145  
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 Db 1873 GTCCTGGAGCTGGAGAGGACTCTGGGTGGCTACTTGGTGGAGGAGCCCAAGCCTTTGCTC 1932

Qy 2146 TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205  
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 Db 1933 TTTAAGGACAGTTACCACAACCTACGCCTCTCCCTCCATGACATCCCCCATGCCCACTGG 1992

Qy 2206 AAGAGTAAGCTCCTTGTGAGTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGC 2265  
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 Db 1993 AGGAGCAAACCTACTGGCCAAGTACCAGGAGATTCCCTTCTACCACGTCTGGAATGGCAGC 2052

Qy	2266	CAGCGGTACTTGCAC TGCACCTTCA CCCTGGAGCTGT CAGCCCCAGCA CTAGTGACCTG	2325
Db	2053	CAGAGAGCCCTGCAC TGCACCTTCA CCCTGGAGAGGCATAGCCTGGCCTCCACGGAGTTC	2112
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2113	ACCTGTAAGGTCTGCGTGCGGCAGGTCGAAGGGGAAGGCCAGATTTTCCAGCTGCACACA	2172
Qy	2386	AACATCACC---AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	ACGTTGGCCGAGACGCCTGCTGGCTCCCTGGATGCTCTCTGCTCTGCCCCGGGCAATGCC	2232
Qy	2443	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCCGGCAGAAGATA	2502
Db	2233	ATCACCACCCAGCTGGGACCCTATGCCTTCAAGATACCCCTGTCCATCCGCCAAAAGATC	2292
Qy	2503	ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA	2562
Db	2293	TGCAGCAGCCTGGACGCCCCCAACTCCCGGGGCAACGACTGGAGGCTGTTGGCGCAGAAG	2352
Qy	2563	CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC	2622
Db	2353	CTGTCCATGGACCGGTACCTAACTACTTCGCCACCAAAGCTAGTCCCACAGGTGTCATC	2412
Qy	2623	CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA	2682
Db	2413	TTAGACCTCTGGGAAGCTCGGCAACAGGATGACGGGGACCTCAACAGCCTGGCCAGTGCC	2472
Qy	2683	GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA	2742
Db	2473	TTGGAGGAGATGGGCAAGAGTGAGATGCTGGTAGCCATGGCCACAGATGGCGATTGCTGA	2532

## RESULT 8

BT758231

LOCUS	BI758231	1034 bp	mRNA	linear	EST 25-SEP-2001
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DEFINITION 603029876F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5200171 5', mRNA sequence.

ACCESSION BI758231

VERSION BI758231.1 GI:15749809

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1034)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL. Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLAM11501 row: g column: 20  
High quality sequence stop: 793.

FEATURES                      Location/Qualifiers  
    source                    1. .1034  
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                              /mol\_type="mRNA"  
                              /db\_xref="taxon:9606"  
                              /clone="IMAGE:5200171"  
                              /lab\_host="DH10B"  
                              /clone\_lib="NIH\_MGC\_114"  
                              /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
                              Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
                              male brains, age range 23-27 yo. Library is oligo-dT  
                              primed and directionally cloned (EcoRV site is destroyed  
                              upon cloning). Average insert size 1.5 kb, insert size  
                              range 1-3 kb. Library is normalized and enriched for  
                              full-length clones and was constructed by C. Gruber  
                              (Invitrogen). Research Genetics tracking code 019. Note:  
                              this is a NIH\_MGC Library."

ORIGIN

Query Match                      27.9%;   Score 768.6;   DB 12;   Length 1034;  
Best Local Similarity            91.2%;   Pred. No. 4.3e-121;  
Matches 918;   Conservative       0;   Mismatches    74;   Indels     15;   Gaps       9;

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Qy      150 GCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACAT 209
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Qy      210 CGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTT 269
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Qy      270 CAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGG 329
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Qy      390 GGTGTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCAC 449
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Qy      570 CATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGA 629
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 Db 601 TGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACCGTGGACCGAGTGGTCCGTCTGC- 659  
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 Db 897 GTGTGCCCAGGTCACTGGACCTGGCACCCGGGA-TGGTCCAGTGAGCTCTGTGT-CCCAC 954  
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 Db 955 GGGTTCTGGCCCTGAGGACTTGGCCTCCTATGTGGGCCTCATCCCG 1001

# RESULT 9

BC033727

LOCUS BC033727 1532 bp mRNA linear HTC 19-NOV-2003

DEFINITION Homo sapiens netrin receptor Unc5h1, mRNA (cDNA clone  
 IMAGE:5166762), containing frame-shift errors.

ACCESSION BC033727

VERSION BC033727.1 GI:21707230

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1532)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1532)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 68 Row: i Column: 2  
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction  
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers

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/db\_xref="taxon:9606"  
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/tissue\_type="Brain, adult medulla"



/clone\_lib="NIH\_MGC\_119"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 26.8%; Score 736.6; DB 11; Length 1532;  
Best Local Similarity 84.2%; Pred. No. 1.5e-115;  
Matches 917; Conservative 0; Mismatches 4; Indels 168; Gaps 1;

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Db      732 CAGAAGGCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCC 791

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Qy      697 AACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCCGCAGCGCCTCCGCTGCTGTC 756
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Qy      817 TGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGG 876

Db     1044 ----- 1043

Qy      877 GGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTA 936

Db     1044 ----- 1043

Qy      937 GACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGG 996
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Db     1044 GACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGG 1103

Qy      997 CGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACT 1056
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Db     1104 CGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACT 1163
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 Db 1284 GTCCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCG 1343  
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 Qy 1237 TCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCC 1296  
 |||  
 Db 1344 TCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCC 1403  
 |||  
 Qy 1297 CATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTC 1356  
 |||  
 Db 1404 CATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTC 1463  
 |||  
 Qy 1357 TGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGC 1416  
 |||  
 Db 1464 TGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGC 1523  
 |||  
 Qy 1417 CCCCTGGGT 1425  
 |||  
 Db 1524 CCCCTGGGT 1532  
 |||

# RESULT 10

AI951556

LOCUS AI951556 788 bp mRNA linear EST 09-MAR-2000

DEFINITION wv36f04.x1 NCI\_CGAP\_Ov18 Homo sapiens cDNA clone IMAGE:2531647 3' similar to TR:008721 008721 TRANSMEMBRANE RECEPTOR UNC5H1. ;, mRNA sequence.

ACCESSION AI951556

VERSION AI951556.1 GI:5743866

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 788)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 1125 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 446.

FEATURES  
source Location/Qualifiers  
1. .788  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2531647"  
/tissue\_type="fibrotheoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NCI\_CGAP\_Ov18"  
/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGACATTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

#### ORIGIN

Query Match 26.7%; Score 735.2; DB 9; Length 788;  
Best Local Similarity 96.5%; Pred. No. 1.9e-115;  
Matches 749; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy      1469 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCGCTCCCTGCCCCGAGGCA 1528
          |||
Db            1 CCGAGGAGTTCGTCTCCCGCCTCTCCGCCCAGAACTACTTCGCTCCCTGCCCCGAGGCA 60

Qy      1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588
          |||
Db            61 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 120

Qy      1589 CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCCGAGGGAAGATCTATGAGATCT 1648
          |||
Db            121 CAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCCCGAGGGAAGATCTATGAGATCT 180

Qy      1649 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC 1708
          |||
Db            181 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC 240

Qy      1709 TGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGG 1768
          |||
Db            241 TGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGG 300

Qy      1769 CTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGT 1828
          |||
Db            301 CTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGT 360

Qy      1829 CGTGCAGGGGAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCT 1888
          |||
Db            361 CGTGCAGGGGAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCT 420

Qy      1889 ACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTG 1948
          |||
```

Db 421 ACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATG 480

Qy 1949 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 2008  
 |||

Db 481 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 540

Qy 2009 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCC 2068  
 |||

Db 541 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGACACTC 600

Qy 2069 ACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGG 2128  
 |||

Db 601 ACGATGCACTCAACGTAGTGGTGCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGG 660

Qy 2129 AGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATG 2188  
 |||

Db 661 AGCCACTGGTACTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATNCATCCACGATG 720

Qy 2189 TGCCACAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGTCAGCTACCAGGAGATCCCTTT 2244  
 |||

Db 721 TGCCACAGCTNCCNTGTGGAGAGTAAGCTTCTTGTGTCAGCTACCCAGAGATCCNCTAT 776

RESULT 11

BX348193/c

LOCUS BX348193 843 bp mRNA linear EST 05-MAY-2003

DEFINITION BX348193 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens  
 cDNA clone CS0DB008YE02 5-PRIME, mRNA sequence.

ACCESSION BX348193

VERSION BX348193.1 GI:30367258

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 3239.r For  
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0BAF004ZD01\\_AF00293\\_1&cluster=3239.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAF004ZD01_AF00293_1&cluster=3239.r).

Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAF004ZD01\_AF00293\_1.

FEATURES Location/Qualifiers

source 1. .843

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DB008YE02"



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|||||
Db      165 CAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAG 106
Qy      2370 CTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGA 2429
|||||
Db      105 CTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGA 46
Qy      2430 GAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCC 2463
|||||
Db      45 GAGTGAAGCGGGGGTCCCAGNCCCTGGTGGGCCC 12

```

# RESULT 12

BI818609

LOCUS BI818609 818 bp mRNA linear EST 04-OCT-2001

DEFINITION 603033362F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5174559 5', mRNA sequence.

ACCESSION BI818609

VERSION BI818609.1 GI:15929902

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 818)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11434 row: 1 column: 16

High quality sequence stop: 744.

FEATURES Location/Qualifiers

source 1..818

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5174559"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_115"

/note="Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 26.0%; Score 716.4; DB 12; Length 818;  
 Best Local Similarity 97.7%; Pred. No. 3.2e-112;  
 Matches 748; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

Qy	43	GCCATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	102
Db	1	GCCATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	60
Qy	103	CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC	162
Db	61	CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC	120
Qy	163	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG	222
Db	121	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG	180
Qy	223	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG	282
Db	181	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG	240
Qy	283	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	342
Db	241	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	300
Qy	343	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTG	402
Db	301	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTG	360
Qy	403	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	462
Db	361	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	420
Qy	463	GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	522
Db	421	GCCTACATCCGCATAGCCATATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	480
Qy	523	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC	582
Db	481	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC	540
Qy	583	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	642
Db	541	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	600
Qy	643	ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC	702
Db	601	ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC	660
Qy	703	ACCTGCGTGGCCAAGAACATCGTGGCACGTC-GCCGCAGCGCCTCCGCTGCTGTATCATCGT	761
Db	661	ACCTGCGTGGCCAAGAACATCGTGGCACGTCAGCCGCAGGGCCTCCGCTGCTGTATCATCGT	720
Qy	762	CTACGTGAACGGTGGGTGGTTCGACG-TGGACCGAGTGGTCCGTCTG	806
Db	721	CTACGTGGACGGCAGCTGGAGCCCGTTGGAGCCAGTGGTCCGGGCTG	766

## RESULT 13

BX364574

LOCUS BX364574 909 bp mRNA linear EST 05-MAY-2003

DEFINITION BX364574 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC023YB10 5-PRIME, mRNA sequence.

ACCESSION BX364574

VERSION BX364574.1 GI:30368812

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 909)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3529.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>[cgi-bin/cluster.cgi?seq=CS1AC006ZF06QP1&cluster=3529.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS1AC006ZF06QP1&cluster=3529.f). Contact :Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS1AC006ZF06QP1.

FEATURES Location/Qualifiers

source

1. .909

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DC023YB10"

/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 25.1%; Score 692; DB 13; Length 909;

Best Local Similarity 99.0%; Pred. No. 5.1e-108;

Matches 703; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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Qy      1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCCCGCGGGCCATGGCCGTCCGGCCC 60
          |||:|||||
Db      201 CCGCRGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCCCGCGGGCCATGGCCGTCCGGCCC 260

Qy      61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
          |||
Db      261 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 320

Qy      121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
```



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      |||
Db      321 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCYAACCCGGACCTGCTTCCCCAC 380
Qy      181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db      381 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 440
Qy      241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
      |||
Db      441 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 500
Qy      301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
      |||
Db      501 GACCACGTGATCGAGCGCA-SACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 559
Qy      361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db      560 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 619
Qy      421 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db      620 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 679
Qy      481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
      |||
Db      680 TATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 739
Qy      541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
      |||
Db      740 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 799
Qy      601 AACGAGGACCTGGTGGACCCGTCCTTGACCCCAATGTATACATCACGCGGGAGCACAGC 660
      |||
Db      800 AACGAGGACCTGGTGGACCCGTCCTTGACCCCAATGTATACATCACGCGGGAGCACAGC 859
Qy      661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 710
      |||
Db      860 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 909

```

#### RESULT 14

AY411748

LOCUS AY411748 2532 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY411748

VERSION AY411748.1 GI:39767716

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2532)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.



Db 433 GCGGCTGGTCCAGCTGGGCAGAGTGGTCGCCCTGCTCCAACCGCTGTGGNNGANNCTGG 492  
 Qy 832 CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAG 891  
 |||| | | | |||| | |||| | || | |||| | | | |||| |  
 Db 493 CAGAAGCGCACCCGGACCTGCACCAACCCGCCCCACTCAACGGAGGGNNNTCTGCGAG 552  
 Qy 892 GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC 951  
 || || | || || | || || | || || | || || | || || |  
 Db 553 GGCCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTCGATGGGGCGTGACG 612  
 Qy 952 CCGTGGAGCAAGTGGTGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC 1011  
 |||| | || || | || || | || || | || || | || || |  
 Db 613 GAGTGGAGCAAGTGGTGCAGCTGCAGCACTGAGTGTGCCCACTGGCGTAGCCGCGAGTGC 672  
 Qy 1012 TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC 1071  
 | || |||| | |||| | || || | || || | || || |  
 Db 673 ATGGCGCCCCCACCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTGCTCGACTCTAAG 732  
 Qy 1072 AACTGTACCAGTGACCTCTGTGTACACAGTGCTTCT----- 1107  
 |||| | | | || | | | | | | | | | | | | | | | |  
 Db 733 AACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAACCTAAGCGACCCCAACAGCCAC 792  
 Qy 1108 -----GGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC---ATCGCCGTGGCCGTC 1155  
 | | | | || | | || | | || | | || | | | | | | | |  
 Db 793 CTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCGTCTTCNTG 852  
 Qy 1156 TGCCTGGTCCTGCTGCTGCTTGCTCCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTG 1215  
 | || | | || | | || | | | | | | | | | | | | | |  
 Db 853 GTCNTGGCAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTC 912  
 Qy 1216 GACTCAGATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATC 1272  
 || | || | | || || | | | | | | | | | | | | | | |  
 Db 913 GACACAGACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTT 972  
 Qy 1273 AAGCCAGCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGC 1326  
 || | | | | || || | || || | | | | | | | | | | |  
 Db 973 AAGACGGCAAGGCCAGCAACCCGAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACA 1032  
 Qy 1327 ACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGG----- 1374  
 || | | | || || || | | | | | | | | | | | | | |  
 Db 1033 GCCAGCGCCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATC 1092  
 Qy 1375 -----CCCCCAAGTTCAGCTCACCA-- 1399  
 | || || | || | | | | | | | | | | | | | | | |  
 Db 1093 CCCATGACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGC 1152  
 Qy 1400 -----ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCC-----ACACA 1440  
 | || | | | | || | | | | | | | | | | | | | | |  
 Db 1153 TCCAGCACTACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGAGTCTTG 1212  
 Qy 1441 CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCTCTCCACCCAG 1500  
 | || | | | | || | | | | | || | | | | | | | | |  
 Db 1213 CCGCTGGCACATAACCTAGCGATTTCGCCCCGGACACCACTTCCTGCACCTGCGCAGC 1272  
 Qy 1501 AACTACTTCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTAT 1545  
 | | | | | | | || || || || | | | | | | | | | |  
 Db 1273 GCCAGCTCGGTTCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGNNAGCAGCGTCAGC 1332

[illegible]

Qy 2386 AACATCACCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG 2442  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2173 ACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCTGGCAGCACT 2232

Qy 2443 GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATA 2502  
 ||| | ||| | |||| | | ||||| ||||| | | ||| | ||||| |  
 Db 2233 GTCACCACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATA 2292

Qy 2503 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2562  
 ||||| | | | ||| |||| | ||||| | | ||| |  
 Db 2293 TGCAACAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAG 2352

Qy 2563 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2622  
 ||| | |||| | | || | ||||| |||| | ||||| | |||| |  
 Db 2353 CTCTCTATGGACCGGTACCTGAATTACTTTGCCACCAAGCGAGCCCCACGGGTGTGATC 2412

Qy 2623 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682  
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 Db 2413 CTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCC 2472

Qy 2683 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742  
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 Db 2473 TTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA 2532

# RESULT 15

BF311804

LOCUS BF311804 934 bp mRNA linear EST 21-NOV-2000

DEFINITION 601897316F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4126706 5', mRNA sequence.

ACCESSION BF311804

VERSION BF311804.1 GI:11259566

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 934)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LLCM1016 row: p column: 03

High quality sequence stop: 707.

FEATURES

source

Location/Qualifiers

1. .934

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4126706"

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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match          24.4%;  Score 672.6;  DB 10;  Length 934;
Best Local Similarity 93.3%;  Pred. No. 1.1e-104;
Matches 747;  Conservative 0;  Mismatches 49;  Indels 5;  Gaps 4;

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Qy      1116 GGACGTGGCCCTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCT 1175
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Qy      1176 TGTCCCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTC 1235
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Qy      1236 GTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCC 1295
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Qy      1296 CCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCT 1355
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Db        182 CCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCACCTACCAGGGCAGTCT 241

Qy      1356 CTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAG 1415
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Db        242 CTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAG 301

Qy      1416 CCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGA 1475
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Db        302 CCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGA 361

Qy      1476 GTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAA 1535
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Db        362 GTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAA 421

Qy      1536 CATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTAT 1595
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Db        422 CATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAAT 481

Qy      1596 CAGCCTCCTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCAC 1655
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Db        482 CAG-CTCCTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCAC 540

Qy      1656 GCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTCC 1715
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Db        541 GCTGCACAAGCCGGAAGACGTGAGGTTG-CCCTAGCTGGCTGTGACACCCTGCTGAGTCC 599

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Qy	1716	CATCGTTAGCTGTGGACCCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCC--TGGCTATG	1773
Db	600	CATCGTTAGCTGTGGACCCCCCTGGCGTCCTGCTCAACCGGGCAGTCATCCCTGGCTAATG	659
Qy	1774	GACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGC	1833
Db	660	GACCACTGTGGGGAGCCAGCCTGACAGTTGGAGCCTGGGCTCAAAAAGGAGTCGGTGC	719
Qy	1834	GAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTAC	1893
Db	720	GAGGGCAGCTGGGA-GATGTGCTGGACTGGGGGAAGAAGGGGGCCTCCACCCTCTATTAT	778
Qy	1894	TGCCAGCTGGAGGCCAGTGCC	1914
Db	779	TGGCAGTGGGAGGCAAGGCC	799

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Job time : 6792 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2004, 14:36:51 ; Search time 10439 Seconds  
(without alignments)  
11426.385 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_ph:\*  
8: gb\_pl:\*  
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10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
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 33: em\_htg\_mus:\*  
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 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2687.4	97.7	2697	6	AX451652	AX451652 Sequence
3	2676.4	97.3	2881	6	AX527916	AX527916 Sequence
4	2356	85.6	3580	6	AX367094	AX367094 Sequence
5	2323.2	84.4	3992	10	MMU487852	AJ487852 Mus muscu
6	2259	82.1	3014	6	BD057524	BD057524 Netrin re
7	2252.2	81.8	2697	6	AX268596	AX268596 Sequence
8	2252.2	81.8	2697	10	RNU87305	U87305 Rattus norv
9	1983.6	72.1	3844	10	BC058084	BC058084 Mus muscu
10	1635.4	59.4	2688	9	BC009333	BC009333 Homo sapi
11	1562.4	56.8	1787	6	BD057525	BD057525 Netrin re
12	1304.2	47.4	9700	6	AX054976	AX054976 Sequence
13	992	36.0	9299	10	MMU72634	U72634 Mus musculu
14	991	36.0	2962	5	AY187310	AY187310 Gallus ga
15	986	35.8	9328	10	AB118026	AB118026 Rattus no
16	970	35.2	3646	9	AF055634	AF055634 Homo sapi
17	943.8	34.3	3770	9	AY126437	AY126437 Homo sapi
18	936.2	34.0	2860	6	AX686445	AX686445 Sequence
19	936.2	34.0	2860	6	AX686447	AX686447 Sequence
20	913.8	33.2	3672	10	BC057560	BC057560 Mus muscu
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22	913.6	33.2	2895	6	AX512281	AX512281 Sequence
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28	892	32.4	4294	10	AK122575	AK122575 Mus muscu
29	875.6	31.8	3788	10	MMU487853	AJ487853 Mus muscu
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31	841.4	30.6	2831	6	BD057526	BD057526 Netrin re
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33	717.2	26.1	2832	5	AY099459	AY099459 Xenopus l

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37	584.2	21.2	3925	10	MMU487854	AJ487854 Mus muscu
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39	583.4	21.2	7002	6	BD162193	BD162193 Novel unc
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43	480.4	17.5	2406	9	AK094595	AK094595 Homo sapi
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# ALIGNMENTS

## RESULT 1

AX449572

LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002

DEFINITION Sequence 1 from Patent WO0210216.

ACCESSION AX449572

VERSION AX449572.1 GI:21698195

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L., Macdougall,J.R. and Smithson,G.

TITLE Proteins and nucleic acids encoding same

JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;

Curagen Corporation (US)

FEATURES

Location/Qualifiers

source

1. .2752

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2752; DB 6; Length 2752;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCGCGGGGCCCCGCGCCCGGGCCCGCCGCGCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC	60

Db	1	CCGCGGGGCCCCGCGCCCGGGCCCGCCGCGCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC	60
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Qy	61	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	120

Db	61	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	120
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Qy	121	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	180

Db	121	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	180
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Qy	181	TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	240
Db	181	TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	240
Qy	241	AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	300
Db	241	AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	300
Qy	301	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC	360
Db	301	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC	360
Qy	361	ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG	420
Db	361	ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG	420
Qy	421	TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCCTACATCCGCATAGCC	480
Db	421	TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCCTACATCCGCATAGCC	480
Qy	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Db	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Qy	541	ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Db	541	ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Qy	601	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
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Qy	661	CTGGTGGTGCGACAGGCCCCGCTTGTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	661	CTGGTGGTGCGACAGGCCCCGCTTGTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Qy	721	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG	780
Db	721	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG	780
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
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Qy	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGCCGG	1200
Db	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
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Db	1321	CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Db	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Db	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Qy	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Db	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Qy	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Db	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Db	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
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Qy	1861	CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920

Db	1861	 CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Qy	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
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Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
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Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2041	 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Qy	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGACAGTTAC	2160
Db	2101	 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGACAGTTAC	2160
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161	 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221	GTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Db	2221	 GTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Qy	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Db	2281	 TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Qy	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
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Qy	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
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Qy	2461	CCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
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Db	2581	 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Qy	2641	CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
Db	2641	 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
Qy	2701	CCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGAGGCCGGCCAG	2752

Db 2701 CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGCCAG 2752

RESULT 2

AX451652

LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002

DEFINITION Sequence 1 from Patent WO0233080.

ACCESSION AX451652

VERSION AX451652.1 GI:21698587

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Koehler, R.H.

TITLE Regulation of human netrin binding membrane receptor unc5h-1

JOURNAL Patent: WO 0233080-A 1 25-APR-2002;

Bayer Aktiengesellschaft (DE)

FEATURES Location/Qualifiers

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/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGGCTC 105
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Db       1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGGCTC 60

Qy     106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
      |||
Db      61 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
      |||
Db     121 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCC GCCACGCAGATCTTCTTCAAGTGCAACGGGGGAG 285
      |||
Db     181 GTGCTGCTTGTGTGCAAGGCCGTGCCC GCCACGCAGATCTTCTTCAAGTGCAACGGGGGAG 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
      |||
Db     241 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTGGAG 405
      |||
Db     301 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
      |||
Db     361 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 420
```

Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGGACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTGGTGGTGGACAGGCCCGCCTTGCTGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTAC	765
Db	661	TGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTAC	720
Qy	766	GTGAACGGTGGGTGGTGGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTGGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGCCCGTGGAGCAAGTGGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAAGTACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAAGTACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCATCTGCTC	1305
Db	1201	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCATCTGCTC	1260

Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1680
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2205



Db	2101	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGTAAGCTCCTTGTTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625
Db	2521	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2580
Qy	2626	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Db	2581	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2640
Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2742
Db	2641	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2697

# RESULT 3

AX527916

LOCUS	AX527916	2881 bp	DNA	linear	PAT 21-NOV-2002
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DEFINITION Sequence 1 from Patent WO0229038.

ACCESSION AX527916

VERSION AX527916.1 GI:25172359

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Herrmann, J.L., Rastelli, L. and Shimkets, R.A.

TITLE Novel proteins and nucleic acids encoding same and antibodies directed against these proteins

JOURNAL Patent: WO 0229038-A 1 11-APR-2002; Curagen Corporation (US)

FEATURES  
source  
Location/Qualifiers  
1. .2881  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 97.3%; Score 2676.4; DB 6; Length 2881;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

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Qy      1  CCGCGGGGGCCCCGCGCCCCGGCCCCGCCCGCTGCCCGCCCCGCGGCCATGGCCGTCCGGCCCC 60
      |||
Db      42  CCGCGGGGGCCCCGCGCCCCGGCCCCGCCCGCTGCCCGCCCCGCGGCCATGGCCGTCCGGCCCC 101

Qy      61  GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
      |||
Db     102  GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 161

Qy     121  CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
      |||
Db     162  CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy     181  TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db     222  TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281

Qy     241  AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
      |||
Db     282  AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 341

Qy     301  GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC 360
      |||
Db     342  GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGGAGCCACCATGGAGGTCCGC 401

Qy     361  ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db     402  ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 461

Qy     421  TGGTGCCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db     462  TGGTGCCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521

Qy     481  AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
      |||
Db     522  AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 581

Qy     541  ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
      |||
Db     582  ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641

Qy     601  AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
      |||
Db     642  AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy     661  CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAAC 720
      |||
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Db	702	CTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	761
Qy	721	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Db	762	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	821
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	822	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	882	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	941
Qy	901	GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGG	957
Db	942	GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG	1001
Qy	958	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1017
Db	1002	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1061
Qy	1018	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1077
Db	1062	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1121
Qy	1078	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1137
Db	1122	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1181
Qy	1138	CTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCTCATCCTCGTTTATTGC	1197
Db	1182	CTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCTCATCCTCGTTTATTGC	1241
Qy	1198	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1257
Db	1242	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1301
Qy	1258	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG	1317
Db	1302	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG	1361
Qy	1318	GACCTCAGCACCAACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1377
Db	1362	GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1418
Qy	1378	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1437
Db	1419	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1478
Qy	1438	AACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1497
Db	1479	AACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1557
Db	1539	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1598

Qy	1558	TTCCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1617
Db	1599	TTCCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1658
Qy	1618	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1677
Db	1659	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1718
Qy	1678	AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT	1737
Db	1719	AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT	1778
Qy	1738	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1797
Db	1779	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1914
Db	1899	CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1958
Qy	1915	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2034
Db	2019	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2078
Qy	2035	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2094
Db	2079	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGAC	2154
Db	2139	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGAC	2198
Qy	2155	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2274
Db	2259	CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2334
Db	2319	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2378
Qy	2335	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2394
Db	2379	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2438

Qy	2395	AAGGACACAAGGTTTGGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2454
Db	2439	AAGGACACAAGGTTTGGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2498
Qy	2455	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2514
Db	2499	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2558
Qy	2515	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2574
Db	2559	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2618
Qy	2575	AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG	2634
Db	2619	AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG	2678
Qy	2635	GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG	2694
Db	2679	GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG	2738
Qy	2695	GGCCAGCCAGACGCTGGCCTCTTCACAGTGTTCGGAGGCTGAGTGCTGAGGCCGGCCAG	2752
Db	2739	GGCCAGCCAGACGCTGGCCTCTTCACAGTGTTCGGAGGCTGAGTGCTGAGGCCGGCCAG	2796

#### RESULT 4

AX367094

LOCUS AX367094 3580 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 13 from Patent WO0198354.

ACCESSION AX367094

VERSION AX367094.1 GI:18855296

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B., Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R., Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O., Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and Sanjanwala,M.S.

TITLE Receptors

JOURNAL Patent: WO 0198354-A 13 27-DEC-2001;

Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers

source 1. .3580

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

/note="Incyte ID No: 6052371CB1"

ORIGIN

Query Match 85.6%; Score 2356; DB 6; Length 3580;

Best Local Similarity 93.6%; Pred. No. 0;

Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

Qy	43	GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	102
Db	1	GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	60
Qy	103	CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAAC	162
Db	61	CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAAC	120
Qy	163	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG	222
Db	121	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG	180
Qy	223	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG	282
Db	181	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG	240
Qy	283	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	342
Db	241	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	300
Qy	343	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTG	402
Db	301	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTG	360
Qy	403	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	462
Db	361	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	420
Qy	463	GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	522
Db	421	GCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	480
Qy	523	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC	582
Db	481	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC	540
Qy	583	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	642
Db	541	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	600
Qy	643	ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC	702
Db	601	ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC	660
Qy	703	ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTC	762
Db	661	ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTC	720
Qy	763	TACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGG	822
Db	721	TACGTG-----	726
Qy	823	CGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCT	882
		-----	
Db	727	-----	726
Qy	883	TTCTGTGAGGGGCAGAAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGC	942

Db	727	-----GACGGC	732
Qy	943	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	1002
Db	733	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	792
Qy	1003	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	1062
Db	793	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	852
Qy	1063	GACACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG	1122
Db	853	GACACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG	912
Qy	1123	GCCCTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTC	1182
Db	913	GCCCTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTC	972
Qy	1183	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1242
Db	973	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1032
Qy	1243	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1302
Db	1033	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1092
Qy	1303	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1362
Db	1093	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1152
Qy	1363	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1422
Db	1153	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1212
Qy	1423	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1482
Db	1213	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1272
Qy	1483	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1542
Db	1273	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1332
Qy	1543	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC	1602
Db	1333	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTC	1392
Qy	1603	CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1662
Db	1393	CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1452
Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1782

Db	1513	AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1572
Qy	1783	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1842
Db	1573	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1632
Qy	1843	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1902
Db	1633	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1692
Qy	1903	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAG	1962
Db	1693	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAG	1752
Qy	1963	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	2022
Db	1753	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	2142
Db	1873	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	1932
Qy	2143	CAC TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	2202
Db	1933	CAC TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2052
Qy	2263	ACGCAGCGGTACTTGCACTGCACCTTCACCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2322
Db	2053	ACGCAGCGGTACTTGCACTGCACCTTCACCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2112
Qy	2323	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2382
Db	2113	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2172
Qy	2383	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2232
Qy	2443	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2502
Db	2233	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2292
Qy	2503	ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA	2562
Db	2293	ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA	2352
Qy	2563	CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC	2622
Db	2353	CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC	2412



Qy	2623	CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA	2682
Db	2413	CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA	2472
Qy	2683	GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA	2742
Db	2473	GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA	2532
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# RESULT 5

MMU487852

LOCUS MMU487852 3992 bp mRNA linear ROD 24-SEP-2002

DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).

ACCESSION AJ487852

VERSION AJ487852.1 GI:22035783

KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1

AUTHORS Engelkamp,D.

TITLE Cloning of three mouse Unc5 genes and their expression patterns at mid-gestation

JOURNAL Mech. Dev. 118 (1-2), 191-197 (2002)

MEDLINE 22239710

PUBMED 12351186

## REFERENCE

2 (bases 1 to 3992)

AUTHORS Engelkamp,D.

TITLE Direct Submission

JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY

## FEATURES

Location/Qualifiers

source

1. .3992  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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gene

1. .3992  
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232. .2928  
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GGAFCEGQNVQKTACATLCPVDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEEC  
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ORIGIN

Query Match 84.4%; Score 2323.2; DB 10; Length 3992;  
 Best Local Similarity 90.3%; Pred. No. 0;  
 Matches 2484; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

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Qy	61	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	120
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Qy	121	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	180
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Qy	361	ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCCGGCTGGAGGAATACTGGTGCCAG	420
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Qy	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Db	667	TATTTGCGCAAGAACTTTGAGCAGGAGCCGCTGGCCAAGGAAGTGCTACTGGAGCAAGGC	726
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Qy	721	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
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Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
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Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
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Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
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Db	1267	AGTGACCTCTGCCTGCACACCTCTTCCGGCCCCGAGGACGTGGCTCTCTACATCGGCCCTC	1326
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCTCGTTTATTGCCGG	1200
Db	1327	GTCGCCGTGGCCGTGTGCCTCATCTTGCTGCTGCTGGTCTCGTCTCATCTACTGCCGC	1386
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Qy	1321	CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
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Qy	1381	CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Db	1567	CCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGCAGTGGCCGCCATACG	1626
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500

Db	1627	CTGCACCACAGCTCCCCACCTCTGAGGCTGAGGACTTCGTCTCCCGCCTCTCCACCCAA	1686	
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Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620	
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Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680	
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Qy	1861	CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920	
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BD057524

LOCUS BD057524 3014 bp DNA linear PAT 27-AUG-2002

DEFINITION Netrin receptors.

ACCESSION BD057524

VERSION BD057524.1 GI:22603130

KEYWORDS JP 2001505062-A/1.

SOURCE synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1 (bases 1 to 3014)

AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.

TITLE Netrin receptors

JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;

THE REGENTS OF THE UNIV OF CALIFORNIA

COMMENT PN JP 2001505062-A/1

PD 17-APR-2001

PF 19-FEB-1998 JP 1998536840

PR 19-FEB-1997 US 08/808982

PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI

PI MASU,

PI KAZUKO KEINO MASU

PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC

Strandedness: Double;

CC Topology: Linear;

FH Key Location/Qualifiers.

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Db	61	CGTGTTTCGGGT	GCCCAGCAGAGTGCCACCGTGGCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCC	ACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCC	ACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGT	GCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGT	GCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGT	TGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGT	CGATCACGTAATTGAACGCAGCACCCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCG	CATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTTCGGGCTGGAG	405
Db	301	ACCATGGAGGTCCG	TATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTTGGGCTGGAG	360
Qy	406	GAATACTGGTGCC	AGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCC	AGTGCGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGC	CAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGC	CCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGG	CATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGG	CATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCG	GAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCG	AAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAG	CCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTACACC	705
Db	601	ACGCGGGAGCACAG	CCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACCTACACC	660
Qy	706	TGCGTGGCCAAGA	ACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTAC	765

Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCATTGTTTAT	720
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Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
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Qy	1066	ACCCGCAACTGTACCAAGTACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAAGTACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGCTGCTGTCTCATC	1185
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Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
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Qy	1366	CAGGATGGGCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
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Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
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Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400



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 Db 2641 GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGCTGTCTGGAGGCCGAGTGTGAGAC 2700  
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# RESULT 7

AX268596

LOCUS AX268596 2697 bp DNA linear PAT 29-OCT-2001

DEFINITION Sequence 15 from Patent WO0175440.

ACCESSION AX268596

VERSION AX268596.1 GI:16541710

KEYWORDS .

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1

AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and  
 Pratt,J.Y.

TITLE Schizophrenia related genes

JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;

WELFIDE CORPORATION (JP)

FEATURES

Location/Qualifiers

source

1. .2697

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/mol\_type="unassigned DNA"

/db\_xref="taxon:10118"

ORIGIN

Query Match 81.8%; Score 2252.2; DB 6; Length 2697;  
 Best Local Similarity 89.7%; Pred. No. 0;  
 Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

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 Db 1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT 60

QY	106	CGCGGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAACCCG	165
Db	61	CGTGGTTTCGGGTGCCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAAACCCC	120
QY	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
QY	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
QY	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTGCATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
QY	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAGGTGTTGGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTCGGGCTGGAG	360
QY	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
QY	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
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Db	481	TCACTGGAGCAAGGCATGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
QY	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
QY	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
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Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
QY	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC	900

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Qy	1006	GAGTGCTCTGACCCAGCACCCCCGCAACGGAGGGGAGGAGTGCCAGGGGACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCCGCAATGGAGGTGAGGAGTGTCTGGGGTGCTGACCTGGAC	1020
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Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCTTGTCGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCCTACCCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAATACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
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Db	1801	 GAGGATGTGCTGCACCTTGGTGAGGAGTACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	 GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
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Qy	2386	AACATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
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Db	2521	 CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC	2580
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ORIGIN

Query Match 81.8%; Score 2252.2; DB 10; Length 2697;  
Best Local Similarity 89.7%; Pred. No. 0;  
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Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
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Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
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Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720

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Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTCGGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTGCTGCTCATC	1185
Db	1081	CTCTACATCGGCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCCTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAATACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560

Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
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Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
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Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGTCCTTCTGTTTGCCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
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Qy	2206	AAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2265
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Qy	2266	CAGCGGTACTTGCACCTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCACCTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505



Db	2401		CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTCCTCATTCGGCAAAAGATCATC	2460
Qy	2506		TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461		GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAACTT	2520
Qy	2566		CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625
Db	2521		CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC	2580
Qy	2626		AACCTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Db	2581		AACCTATGGGAGGCACGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG	2640
Qy	2686		GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGCTGA	2742
Db	2641		GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTGCGAGGCCGAGTGTTGA	2697

# RESULT 9

BC058084

LOCUS BC058084 3844 bp mRNA linear ROD 21-OCT-2003

DEFINITION Mus musculus unc-5 homolog A (C. elegans), mRNA (cDNA clone MGC:66671 IMAGE:6813463), complete cds.

ACCESSION BC058084

VERSION BC058084.1 GI:34784158

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3844)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3844)

AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 126 Row: b Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES Location/Qualifiers  
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/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="MGC:66671 IMAGE:6813463"  
/tissue\_type="Brain, mouse, 13.5, 14.5, 16.5, 17.5 dpc"  
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/note="Vector: pYX-ASC"  
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ORIGIN

[illegible]

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Qy	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Db	687	TATTTGCGCAAGAACTTTGAGCAGGAGCCGCTGGCCAAGGAAGTGTCACTGGAGCAAGGC	746
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Db	747	ATTGTGCTACCTTGTGCGCCCCCGGAAGGAATCCCCCAGCTGAGGTGGAGTGGCTCCGA	806
Qy	601	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Db	807	AATGAGGACCTCGTGGACCCCTCCCTCGACCCCAATGTGTACATCACACGGGAGCACAGC	866
Qy	661	CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAAC	720
Db	867	CTAGTCGTGCGGCAGGCCCCGCTGGCCGACACTCCCAACTACACCTGCGTGGCCAAGAAC	926
Qy	721	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGG	780
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Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
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Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	975	-----	974
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
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Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
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Qy	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1059	GCGCCCCGCAACGGAGGTGAGGAGTGCCGGGGTGCTGACCTGGACACCCGCAACTGTACC	1118
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1119	AGTGACCTCTGCCTGCACACCTCTCCGGCCCCGAGGACGTGGCTCTCTACATCGGCCTC	1178
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCTCGTATTATGCGCG	1200
Db	1179	GTCGCCGTGGCCGTGTGCCTCATCTTGCTGCTGCTGGTCCTCGTCCTCATCTACTGCCGC	1238
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1239	AAGAAGGAAGGACTGGACTCAGACGTGGCTGACTCATCCATCCTTACCTCAGGCTTCCAG	1298

Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1299	CCTGTCAGCATCAAGCCCAGCAAAGCAGACAATCCCCATCTGCTCACCATCCAACCGGAC	1358
Qy	1321	CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1359	CTCAGCACCACCACGACCACCTACCAGGGCAGCCTGTGTCCCCGGCAGGATGGACCCAGC	1418
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Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
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Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCAC TGTGGGGAGCCCAGCCCTGAC	1800
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Db	1959	GTCTTTACCGAGCAGCTAGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	2018
Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
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Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
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Db	2139	AAGCAGCTGGGTGGACAGCTGATCCAGGAGCCCCGTGTCTTGCACTTCAAAGACAGTTAC	2198
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2199	CACAACCTACGTCTGTCCATCCACGACGTGCCAGCTCCCTGTGGAAGAGCAAGCTCCTT	2258
Qy	2221	GTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGAC	2280
Db	2259	GTCAGCTACCAGGAGATCCCTTTTACCACATCTGGAATGGCACTCAGCAGTATCTGCAC	2318
Qy	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Db	2319	TGCACCTTCACCCTGGAGCGCGTCAATGCCAGCACCAGCGACCTGGCCTGCAAGGTGTGG	2378
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Qy	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
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Db	2559	CCCTGCAGCCGGGGCGCCGACTGGCGAACTCTAGCCAGAACTTCACCTGGACAGCCAT	2618
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Qy	2641	CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
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# RESULT 10

BC009333

LOCUS BC009333 2688 bp mRNA linear PRI 19-DEC-2003

DEFINITION Homo sapiens cDNA clone IMAGE:4126760, partial cds.

ACCESSION BC009333

VERSION BC009333.2 GI:40226527

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2688)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE 2 (bases 1 to 2688)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT On Dec 19, 2003 this sequence version replaced gi:14424611.  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 26 Row: g Column: 22.

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/db\_xref="taxon:9606"

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Matches 1636; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1176 TGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTC 1235
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Db 61 TGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTC 120
QY 1236 GTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCC 1295
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Db 121 GTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCC 180
QY 1296 CCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCT 1355
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Db 181 CCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCT 240
QY 1356 CTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAG 1415
|
Db 241 CTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAG 300
QY 1416 CCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGA 1475
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Qy	1596	CAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAC	1655
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Qy	1656	GCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCC	1715
Db	541	GCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCC	600
Qy	1716	CATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGA	1775
Db	601	CATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGA	660
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Db	841	GGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGT	900
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Db	901	GGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGC	960
Qy	2076	ACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACG	2135
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# RESULT 11

BD057525

LOCUS BD057525 1787 bp DNA linear PAT 27-AUG-2002

DEFINITION Netrin receptors.

ACCESSION BD057525

VERSION BD057525.1 GI:22603131

KEYWORDS JP 2001505062-A/2.

SOURCE synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1 (bases 1 to 1787)

AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.

TITLE Netrin receptors

JOURNAL Patent: JP 2001505062-A 2 17-APR-2001;

THE REGENTS OF THE UNIV OF CALIFORNIA

COMMENT PN JP 2001505062-A/2

PD 17-APR-2001

PF 19-FEB-1998 JP 1998536840

PR 19-FEB-1997 US 08/808982

PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI

PI MASU,

PI KAZUKO KEINO MASU

PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC

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Matches 1661;  Conservative 0;  Mismatches 16;  Indels 9;  Gaps 8;

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Qy      1489 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG 1548
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# RESULT 12

AX054976

LOCUS AX054976 9700 bp DNA linear PAT 13-JAN-2001

DEFINITION Sequence 91 from Patent WO0073328.

ACCESSION AX054976

VERSION AX054976.1 GI:12228344

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1

AUTHORS van Criekinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.

TITLE Unc-5 constructs and screening methods

JOURNAL Patent: WO 0073328-A 91 07-DEC-2000;  
Devgen NV (BE)

FEATURES

source

Location/Qualifiers

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Query Match 47.4%; Score 1304.2; DB 6; Length 9700;  
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Qy      1557 CTTCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGA 1616
Db      127 CTTCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCAGA 186
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Qy	2037	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	2096
Db	607	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	666
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Qy	2217	CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCGCGGTACTT	2276
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Qy	2277	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	2336
Db	847	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	906
Qy	2337	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	2396
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Qy	2397	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT	2456
Db	967	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCAAGCCCTGGT	1026
Qy	2457	GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	2516
Db	1027	GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	1086

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Qy      2517 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG 2576
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Qy      2577 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 2636
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Qy      2637 GGC GCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 2696
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Db      1207 GGC GCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 1266

Qy      2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGC 2745
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Db      1267 CCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGTC 1315

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# RESULT 13

MMU72634

LOCUS MMU72634 9299 bp mRNA linear ROD 13-MAY-1997

DEFINITION Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.

ACCESSION U72634

VERSION U72634.1 GI:2088526

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 9299)

AUTHORS Ackerman,S.L., Kozak,L.P., Przyborski,S.A., Rund,L.A., Boyer,B.B. and Knowles,B.B.

TITLE The mouse rostral cerebellar malformation gene encodes an UNC-5-like protein

JOURNAL Nature 386 (6627), 838-842 (1997)

MEDLINE 97271898

PUBMED 9126743

REFERENCE 2 (bases 1 to 9299)

AUTHORS Ackerman,S.L., Kozak,L.P., Rund,L.A. and Knowles,B.B.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-1996) The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA

FEATURES Location/Qualifiers

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source      1. .9299
              /organism="Mus musculus"
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              /map="between Amy1 and Mpmv9"

gene        1. .9299
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CDS         151. .2946
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Db 728 GGATCCCAGTGGCTGAGGTGGAATGGCTAAAGAATGAAGACATAATTGATCCTGCTGAAG 787

Qy 629 ACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGGACAGGCCCGCCTTGCTG 688  
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Db 788 ATCGGAACCTTTTATATTACTATCGATCACAACCTGATCATCAAGCAAGCCCGACTCTCAG 847

Qy 689 ACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCGCCTCCG 748  
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Db 848 ATACAGCAAATTATACCTGTGTTGCCAAAAATATTGTTGCCAAGAGAAAAAGCACCACAG 907

Qy 749 CTGCTGTTCATCGTCTACGTGAACGGTGGGTGGTGGACGTGGACCGAGTGGTCCGTCTGCA 808  
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Db 908 CCACTGTTCATCGTGTATGTTAATGGTGGCTGGTCCACCTGGACAGAGTGGTCTGTGTGTA 967

Qy 809 GCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTC 868  
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Db 968 ACAGCCGCTGTGGGCGAGGATATCAGAAACGCACAAGAACCTGCACCAACCCAGCCCCAC 1027

Qy 869 TCAACGGGGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCCTGT 928  
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Db 1028 TCAATGGTGGGCGCTTTCTGTGAGGGGCGAGTGTGCAGAAAATAGCATGCACTACGTTAT 1087

Qy 929 GCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCA 988  
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Db 1088 GTCCAGTGGATGGTAGGTGGACTTCATGGAGCAAATGGTCAACCTGTGGGACTGAATGCA 1147

Qy 989 CCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCC 1048  
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Db 1148 CCCACTGGCGCAGGAGGGAGTGTACAGCACCAGCCCCAAGAACGGGGGTAAGGACTGTG 1207

Qy 1049 AGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTG 1108  
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Db 1208 ATGGCCTGGTCTTCCAATCCAAGAACTGCACTGATGGGCTGTGCATGCAGGCTGCTCCTG 1267

Qy 1109 GCCCTGAGGACGTGGCCCTCTATGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCC 1165  
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Db 1268 ACTCAGATGATGTGGCTCTCTACGTGGGGATTGTGATCGCTGTAACAGTCTGTCTGGCGA 1327

Qy 1166 TGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATG 1225  
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Db 1328 TCACTGTTGTGGTGGCCCTGTTTGTGTATCGGAAGAACCACCGTGACTTTGAGTCTGACA 1387

Qy 1226 TGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAG 1285  
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Db 1388 TCATTGACTCCTCAGCACTCAATGGCGGCTTTTCAAGCTGTGAACATCAAG-----G 1438

Qy 1286 CAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACC 1345  
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Db 1439 CTGCCAGACAAGATCTCCTGGCTGTCCCCCTGACCTCACCTCAGCTGCAGCCATGTACA 1498

Qy 1346 AGGGCAGTCTCTGTCCCCGGCAGGATG-----GGCCCAGCCCCAAGTTCCAGCTCACCAA 1400  
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Db 1499 GGGGACCTGTCTATGCTCTGCATGATGTCTCAGACAAAATCCCAATGACCAACTCTCCAA 1558

Qy 1401 TGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCAC 1460  
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Db 1559 TTCTGGACCCACTACCCAACCTTGAAAATCAAAGTGTACAACAGCTCAGGTGCTGTCACTC 1618

Qy 1461 CTC-----TGAGGCCGAGGAGTTCTGTCTCCCGCCTCTCCACCC----- 1498  
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 Db 1619 CTCAGGATGACCTTGCCGAGTTCTCATCCAAACTGTCACCCAGATGACCCAGTCCTTGC 1678

Qy 1499 -----AGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCA 1534  
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Qy 1655 CGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTC 1714  
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Qy 1715 CCATCGTTAGCTGTGGACCCCTGGCGTCTCTGCTCACCCGGCCAGTCATCCTGGCTATGG 1774  
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 Db 1979 ATCACTGTGCAGACCCAGCACCGAGGACTGGAAGATCCAGCTCAAAAACCAGGCAGTGC 2038

Qy 1835 AGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGCGCCCTCCCACCTCTACTACT 1894  
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 Db 2219 TCTGCTGCTCTTCCCTGGAGTACAGCATTAGAGTCTACTGCCTGGATGACACACAGGATG 2278

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Qy 2195 GCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCT 2254  
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 Db 2459 GGAGTGGCTCTCAAAGAAACCTCCACTGCACCTTCACTCTGGAAAGACTCAGCCTAAACA 2518  
 Qy 2315 CTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCA 2374  
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 Db 2519 CAGTGGAAGTGGTTTGCAACTCTGTGTGCGGCAGGTTGAAGGAGAAGGGCAGATCTTCC 2578  
 Qy 2375 GCATCAACTTCAACATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTG 2434  
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 Db 2579 AGCTCAACTGTACTGTGTGAGAGGAACCTACTGGCATCGACTTACCTCTCCTGGACCCTG 2638  
 Qy 2435 AAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCCGGC 2494  
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 Db 2639 CTAGTACCATCACCACTGTCAACGGACCAAGTGCTTTGAGCATTCTCTCCCTATCCGGC 2698  
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 Qy 2675 CTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTG 2734  
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 Db 2879 CAGCCGTCCTGGAAGAAATGGGAAGACATGAGACAGTGGTGTCTTGGCAGCAGAAGGAC 2938  
 Qy 2735 AGTGCTGA 2742  
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 Db 2939 AGTATTGA 2946

# RESULT 14

AY187310

LOCUS AY187310 2962 bp mRNA linear VRT 06-JUN-2003

DEFINITION Gallus gallus UNC5-like protein 3 mRNA, complete cds.

ACCESSION AY187310

VERSION AY187310.1 GI:31442350

KEYWORDS .

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 2962)

AUTHORS Guan,W. and Condic,M.L.

TITLE Characterization of Netrin-1, Neogenin and cUNC-5H3 expression  
 during chick dorsal root ganglia development

JOURNAL Gene Expr. Patterns 3, 369-373 (2003)

REFERENCE 2 (bases 1 to 2962)

AUTHORS Guan,W. and Condic,M.L.

TITLE Direct Submission

JOURNAL Submitted (26-NOV-2002) Neurobiology & Anatomy, University of Utah,  
20 North, 1900 East, Salt Lake City, UT 84132-3401, USA

FEATURES Location/Qualifiers  
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CDS 1. .2796  
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#### ORIGIN

Query Match 36.0%; Score 991; DB 5; Length 2962;  
Best Local Similarity 62.6%; Pred. No. 1.7e-156;  
Matches 1662; Conservative 0; Mismatches 930; Indels 63; Gaps 5;

Qy 149 TGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACA 208  
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Db 158 TTCCTTCTGATCCTCCAGAGCCATTGCCCACTTTCTCATTGAACCCGAAGAAGCTTACA 217

Qy 209 TCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCT 268  
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Qy 269 TCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACG 328  
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Db 278 TTAAGTGCAACAGTGAATGGGTTTCATCAGAAGGATCATGTGGTGGATGAGAGAGTAGATG 337

Qy 329 GGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGA 388  
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Db 338 AAACCTCTGGTCTGATCGTCTGTGAGGTGAGCATCGAGATTTCCCGCCAGCAGGTGGAAG 397

Qy 389 AGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCA 448  
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Db 398 AGCTCTTTGGACCCGAGGACTACTGGTGCCAGTGTGTGCGCTGGAGCTCAGCTGGCACCA 457

Qy 449 CCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGC 508  
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Db 458 CCAAGAGCCGCAAGGCCTACGTCCGCATTGCATATCTCAGAAAGACTTTTGAGCAGGAGC 517

Qy 509 CGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGG 568  
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Db 518 CGCTGGGGAAAGAAGTGTCCCTGGAGCAAGAGGTCTGCTCCAGTGCCGTCTCTCTGAAG 577

Qy 569 GCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGG 628  
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Db 578 GCATTCAGTAGCTGAGGTAGAGTGGCTGAAGAATGAAGAGGTGATCGATCCTGTGGAAG 637

Qy 629 ACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTG 688  
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Db 638 ACCGAAATTTTACATCACCATTGATCACAACCTGATCATCAAGCAAGCCCGGCTTTCCG 697

Qy 689 ACACGGCCAACCTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGACGCGCTCCG 748  
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Db 698 ACACGGCTAACTACACCTGTGTGGCCAAAACATTGTGGCCAAAAGGAAAAGCACGACAG 757

Qy 749 CTGCTGTCATCGTCTACGTGAACGGTGGGTGGTGCACGTGGACCGAGTGGTCCGTCTGCA 808  
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Db 758 CAACTGTGATTGTCTATGTGAATGGAGGCTGGTCTACCTGGACCGAGTGGTCAGCGTGCA 817

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Qy 869 TCAACGGGGGCGCTTTCTGTGAGGGGCGAATGTCCAGAAAACAGCCTGCGCCACCCTGT 928  
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Db 878 TCAATGGGGGGGCTTCTGCGAGGGGCAAATGTTCAAGAAATAGCTTGCAACCACCCTGT 937

Qy 929 GCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCTGTGGGCTGGACTGCA 988  
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Db 938 GTCCAGTGGATGGCAAATGGACGTCTGGAGCAAGTGGTCCACTTGTGGCACAGAGTGTA 997

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Qy 1049 AGGGCACTGACCTGGACACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTG 1108  
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Db 1058 AGGGACTGGTGTGCTGCAGTCTAAGAACTGCACTGATGGGCTCTGCATGCAGGCTGCACCTG 1117

Qy 1109 GCCCTGAGGACGTGGCCCTCTATGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCC 1165  
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Db 1118 ACTCGGATGATGTTGCTCTCTACGTGGGGATTGTCAATTGCTGTGATTGTGTGCCTGGCTA 1177

Qy 1166 TGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATG 1225  
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Db 1178 TTTCTGTGGTTGTGGCCCTGTTTGTCTATCGCAAGAACCACCGTGACTTTGAGTCAGATA 1237

Qy 1226 TGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAG 1285  
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Db 1238 TTATCGACTCATCGGCGCTAAATGGGGGATTTAGCCTGTAAACATCAAGGCTGCAAGAC 1297

Qy 1286 CAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACC 1345  
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Db 1298 AAGAC-----CTCTTGGCAGTGCCACCAGACCTCACTTCTGCTGCAGCCATGTACA 1348

Qy	1346	AGGGCAGTCTCTGTCCCCGGCAGGATG-----GGCCCAGCCCCAAGTTCCAGCTCACCAA	1400
Db	1349	GGGGGCCTGTGTATGCCTTGCATGATGTCTCTGATAAAATCCCAATGACCAATTCTCCGA	1408
Qy	1401	T----GGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTC	1456
Db	1409	TCCTGGACCCACTGCCCAATCTGAAGATTAAAGTTTATAACACCTCTGGAGCAGTCACCC	1468
Qy	1457	CCACCTCTGAGGCCGAGGAGTTTCGTCTCCCGCCTCTCCACCC-----	1498
Db	1469	CCCAGGATGAACTCTCTGACTTCTCCTCCAAGCTGTCCCCACAGATTACCCAGTCTCTGT	1528
Qy	1499	-----AGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCA	1534
Db	1529	TGGAGAATGAGACTCTGAACGTGAAGAACCAAAGCCTTGCACGGCAAACAGACCCATCCT	1588
Qy	1535	ACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTA	1594
Db	1589	GCACTGCATTTGGGACCTTCAACTCGTTAGGGGGCCACCTAGTAATTCCTAATTCAGGAG	1648
Qy	1595	TCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCA	1654
Db	1649	TGAGCTTGCTGATCCCAGCAGGGGCTGTCCCCAAGGAAGAGTCTATGAAATGTATGTGA	1708
Qy	1655	CGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTC	1714
Db	1709	CAGTCCACAGGAAGGAGGGCATGAGACCACCTGTAGAAGACAGCCAGACGCTGCTGACAC	1768
Qy	1715	CCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGG	1774
Db	1769	CAGTGGTGAGCTGTGGCCACCAGGAGCGCTGCTGACCCGACCGTTGTGCTGACCATGC	1828
Qy	1775	ACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCG	1834
Db	1829	ACCACTGTGCTGAGCCCAACATGGATGACTGGCAGATCCAGCTCAAGCACCAGGCAGGCC	1888
Qy	1835	AGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGCGCCCTCCCACCTCTACTACT	1894
Db	1889	AGGGACCATGGGAGGATGTAGTGGTGGTGGGGAGGAAAACCTCACCACCTCATGCTACA	1948
Qy	1895	GCCAGCTGGAGGCCAGTGCCTGCTACGTCTTACCGAGCAGCTGGGCGCCTTTGCCCTGG	1954
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# RESULT 15

AB118026

LOCUS AB118026 9328 bp mRNA linear ROD 19-DEC-2003

DEFINITION Rattus norvegicus Unc5h3 mRNA, complete cds.

ACCESSION AB118026

VERSION AB118026.1 GI:40217509

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

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REFERENCE 1
AUTHORS Kuramoto,T., Kuwamura,M. and Serikawa,T.
TITLE Rat neurological mutations cerebellar vermis defect and hobble are
caused by mutations in the netrin-1 receptor gene Unc5h3
JOURNAL Mol. Brain Res. (2003) In press
REFERENCE 2 (bases 1 to 9328)
AUTHORS Kuramoto,T. and Serikawa,T.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2003) Takashi Kuramoto, Institute of Laboratory
Animals, Graduate School of Medicine, Kyoto University;
Yoshidakonoe-cho, Sakyo-ku, Kyoto 606-8501, Japan
(E-mail:tkuramot@anim.med.kyoto-u.ac.jp,
URL:www.anim.med.kyoto-u.ac.jp, Tel:81-75-753-4494,
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Query Match             35.8%;  Score 986;  DB 10;  Length 9328;
Best Local Similarity   62.7%;  Pred. No. 1e-155;
Matches 1651;  Conservative 0;  Mismatches 920;  Indels 63;  Gaps 5;

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Qy	1240	ATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCAT	1299
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Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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#### ALIGNMENTS

##### RESULT 1

ABK37922

ID ABK37922 standard; cDNA; 2752 BP.

XX

AC ABK37922;

XX

DT 21-MAY-2002 (first entry)

XX

DE cDNA encoding Human protein NOV1.

XX

KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;  
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;  
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;  
KW psychosis; neurological disorder; anxiety; schizophrenia;  
KW manic depression; dementia; dyskinesia; Huntington's disease;  
KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.

PR 15-AUG-2000; 2000US-0225470P.

PR 16-AUG-2000; 2000US-0225697P.

PR 01-FEB-2001; 2001US-0263662P.

PR 05-APR-2001; 2001US-0281645P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;  
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;

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DR WPI; 2002-180074/23.

DR P-PSDB; AAU85403.

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PT New isolated cytoplasmic, nuclear, membrane bound, or secreted  
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,  
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and  
PT immune disorders.

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PS Claim 9; Page 9-10; 213pp; English.

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CC The invention relates to an isolated cytoplasmic, nuclear, membrane  
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature  
CC form. Also included are the nucleic acids encoding the NOVX proteins, a  
CC vector comprising the nucleic acid, a cell comprising the vector, an anti  
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the  
CC antibody are useful for treating or preventing a NOVX-associated  
CC disorder, where the disorder is selected from cardiomyopathy,  
CC atherosclerosis, diabetes, a disorder related to cell signal processing  
CC and metabolic pathway modulation, metabolic disorders, obesity,  
CC infectious disease, anorexia, cancer-associated cachexia, cancer,  
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,  
CC immune disorders, haematopoietic disorders, and the various  
CC dyslipidaemias, metabolic disturbances associated with obesity, the  
CC metabolic syndrome X and wasting disorders associated with chronic

CC diseases, bacterial, fungal, protozoal and viral infections, pain,  
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's  
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina  
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic  
CC hypertrophy, and psychotic and neurological disorders, including anxiety,  
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,  
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The  
CC nucleic acid is useful in gene therapy. The present sequence encodes a  
CC NOVX protein

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SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Query Match 100.0%; Score 2752; DB 6; Length 2752;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCCCGCGGGCCATGGCCGTCCGGCCC 60
      |||
Db      1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCCCGCGGGCCATGGCCGTCCGGCCC 60

Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
      |||
Db     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120

Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
      |||
Db    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

Qy    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
      |||
Db    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
      |||
Db    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360

Qy    361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db    361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420

Qy    421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db    421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy    481 AGATTGCGCAAGAAGTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCTTGGAGCAGGGC 540
      |||
Db    481 AGATTGCGCAAGAAGTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCTTGGAGCAGGGC 540

Qy    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
      |||
Db    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600

Qy    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
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Db	601	 AACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Qy	661	CTGGTGGTGGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	661	 CTGGTGGTGGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Qy	721	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Db	721	 ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	781	 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	841	 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Db	961	 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Qy	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Db	1141	 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1261	 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Qy	1321	CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1321	 CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Db	1381	 CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500

Db	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Qy	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Db	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Qy	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCCTGGC	1740
Db	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Db	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Db	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Qy	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Db	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Qy	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Db	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Db	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Qy	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTCAAGGACAGTTAC	2160
Db	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTCAAGGACAGTTAC	2160
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Db	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Qy	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Db	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340

Qy	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Db	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Qy	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Db	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Qy	2461	CCCAGTGCCTTCAAGATCCCCCTTCCTCATTTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Db	2461	CCCAGTGCCTTCAAGATCCCCCTTCCTCATTTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Qy	2521	CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580
Db	2521	CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580
Qy	2581	CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Db	2581	CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Qy	2641	CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
Db	2641	CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
Qy	2701	CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG	2752
Db	2701	CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG	2752

✓  
RESULT 2  
ABK52891  
ID ABK52891 standard; DNA; 2697 BP.  
XX  
AC ABK52891;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.  
XX  
KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;  
KW nootropic; neuroprotective; cytostatic; antiparkinsonian;  
KW cerebroprotective; cancer; central nervous system; CNS; stroke;  
KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .2697  
FT /\*tag= a  
FT /product= "Netrin binding membrane receptor UNC5H-1"  
XX  
PN WO200233080-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 15-OCT-2001; 2001WO-EP011891.

XX  
PR 16-OCT-2000; 2000US-0240061P.

XX  
PA (FARB ) BAYER AG.

XX  
PI Koehler RH;

XX  
DR WPI; 2002-463314/49.  
DR P-PSDB; AAU97899.

XX  
PT Novel human netrin binding membrane receptor polypeptide and  
PT polynucleotides for identifying modulating agents useful in treating  
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,  
PT Alzheimer's disease.

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PS Claim 1; Fig 1; 94pp; English.

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CC This invention relates to the DNA and protein sequences of a novel  
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA  
CC sequence of the invention is useful as a probe for detecting a nucleic  
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences  
CC of the invention are useful to screen for agents which decrease the  
CC activity of the UNC5H-1 protein. The sequences are also useful for  
CC screening agents which regulate (modulate) the activity of the protein of  
CC the invention. A pharmaceutical composition containing the protein of the  
CC invention or a reagent that modulates the activity of the UNC5H-1 protein  
CC may be useful for treating a UNC5H-1 dysfunction related disease such as  
CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's  
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion  
CC proteins comprising the UNC5H-1 protein are useful for generating  
CC antibodies and for in various assay systems, and the protein can be used  
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method  
CC of the invention is useful for detecting a coding sequence for the UNC5H-  
CC 1 protein. The present sequence represents a DNA sequence encoding the  
CC human netrin binding membrane receptor UNC5H-1 protein of the invention

XX  
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	46	ATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	105
Db	1	ATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	60
Qy	106	CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCG	165
Db	61	CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCG	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAAGCCA	225
Db	121	GACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAAGCCA	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	240

Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGCATAGCCATATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGGCAGAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTGGTGGTGGCAGAGGCCCGCCTTGCTGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTTCATCGTCTAC	765
Db	661	TGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTTCATCGTCTAC	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGCCCGTGGAGCAAGTGGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1080

Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCTCATC	1185
Db	1081	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCTCATC	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1680
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025

Db	1921	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2205
Db	2101	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625
Db	2521	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2580
Qy	2626	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Db	2581	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2640
Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2742
Db	2641	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2697

RESULT 3

ABK49422

ID ABK49422 standard; DNA; 2881 BP.

XX

AC ABK49422;

XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE DNA encoding human UNC5-like protein NOV1.  
 XX  
 KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;  
 KW cell signal processing; metabolic pathway modulation; cancerous tissue;  
 KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;  
 KW chromosome 13; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 87..2786  
 FT /\*tag= a  
 FT /product= "Human UNC5-like protein NOV1"  
 XX  
~~PN~~ WO200229038-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 04-OCT-2001; 2001WO-US031377.  
 XX  
 PR 04-OCT-2000; 2000US-0237862P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Herrmann JL, Rastelli L, Shimkets RA;  
 XX  
 DR WPI; 2002-340104/37.  
 DR P-PSDB; AAU79939.  
 XX  
 PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for  
 PT treating cardiomyopathy, atherosclerosis, and cancer.  
 XX  
 PS Claim 8; Page 7-8; 180pp; English.  
 XX  
 CC The present invention relates to a new NOVX polypeptide having a 900  
 CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)  
 CC residue amino acid sequence, as given in the specification. The novel  
 CC polypeptide, and its encoding polynucleotide, are used to treat  
 CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell  
 CC signal processing and metabolic pathway modulation, in a human. Detecting  
 CC the polypeptide or polynucleotide is useful for identifying cancerous  
 CC tissue. The antibody can be used to treat diabetes or cancer. The host  
 CC cells can be used to produce non-human transgenic animals useful in drug  
 CC screening. The present nucleic acid sequence is that of the human UNC5-  
 CC like NOV1 gene located on chromosome 13. This sequence encodes the human  
 CC UNC5-like protein NOV1 of the invention  
 XX  
 SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;  
  
 Query Match 97.3%; Score 2676.4; DB 6; Length 2881;  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

Qy 1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCCC 60



Db	42	 CCGCGGGGCCCCGCGCCCGGCCCCCGCCTGCCCCGCCCCGCGGCCATGGCCGTCCGGCCC	101
Qy	61	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	120
Db	102	 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	161
Qy	121	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	180
Db	162	 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	221
Qy	181	TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	240
Db	222	 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	281
Qy	241	AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	300
Db	282	 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	341
Qy	301	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC	360
Db	342	 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC	401
Qy	361	ATTAATGTCTCAAGGCAGCAGGTGCGAGAAAGTGTTCGGGCTGGAGGAATACTGGTGCCAG	420
Db	402	 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAAGTGTTCGGGCTGGAGGAATACTGGTGCCAG	461
Qy	421	TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC	480
Db	462	 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC	521
Qy	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Db	522	 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	581
Qy	541	ATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Db	582	 ATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	641
Qy	601	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Db	642	 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	701
Qy	661	CTGGTGGTGCACAGGCCCCGCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	702	 CTGGTGGTGCACAGGCCCCGCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	761
Qy	721	ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG	780
Db	762	 ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG	821
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	822	 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900

[illegible]

Qy	1738	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1797
Db	1779	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1914
Db	1899	CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1958
Qy	1915	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2034
Db	2019	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2078
Qy	2035	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2094
Db	2079	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC	2154
Db	2139	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC	2198
Qy	2155	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTCAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2274
Db	2259	CTCCTTGTCAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2334
Db	2319	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2378
Qy	2335	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2394
Db	2379	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2438
Qy	2395	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2454
Db	2439	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2498
Qy	2455	GTGGGCCCCAGTGCCTTCAAGATCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2514
Db	2499	GTGGGCCCCAGTGCCTTCAAGATCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2558
Qy	2515	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2574
Db	2559	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2618

Qy 2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634  
 |||  
 Db 2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678  
 Qy 2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694  
 |||  
 Db 2679 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2738  
 Qy 2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752  
 |||  
 Db 2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2796

#### RESULT 4

AAK52261

ID AAK52261 standard; cDNA; 2907 BP.

XX

AC AAK52261;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polynucleotide SEQ ID NO 806.

XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation; ss.

XX

OS Homo sapiens.

XX

PN WO200157190-A2.

XX

PD 09-AUG-2001.

XX

PF 05-FEB-2001; 2001WO-US004098.

XX

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX

DR WPI; 2001-476283/51.

DR P-PSDB; AAM79128.

XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful

PT in diagnosis and gene therapy.

XX

XX

XX

Qy 572 TCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACC 631  
| | | | | | | | | | | | | | | | | | | | | |  
Dh 650 TCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACC 709

Db

Qy	632	CCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCCGCTTGCTGACA	691
Db	710	CCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCCGCTTGCTGACA	769
Qy	692	CGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGAGCGCCTCCGCTG	751
Db	770	CGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGAGCGCCTCCGCTG	829
Qy	752	CTGTCATCGTCTAC-----	765
Db	830	CTGTCATCGTCTACGGTGGGCCCCGGGACTCCCTGGTCACAGGGAGAGGCACTGCGGTGC	889
Qy	766	-----GTGAACGGTGGGTGGTTCGA	784
Db	890	CCCTGGGCAGTGACATGTGGCTGTCCTTCTCTGTCCGGCCAGTGAACGGTGGGTGGTTCGA	949
Qy	785	CGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCC	844
Db	950	CGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCC	1009
Qy	845	GGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCC	904
Db	1010	GGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCC	1069
Qy	905	AGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGT	964
Db	1070	AGAAAACAGCCTGCGCCACCCTGTGCCCAGTGGACGGCAGCTGGAGCCCGTGGAGCAAGT	1129
Qy	965	GGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCAC	1024
Db	1130	GGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCAC	1189
Qy	1025	CCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTG	1084
Db	1190	CCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTG	1249
Qy	1085	ACCTCTGTGTACACA-----	1099
Db	1250	ACCTCTGTGTACACAACCTACACCCCTGCCCCACCAAGGCCATGCTGTCTCCCGCAG	1309
Qy	1100	GTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCC	1159
Db	1310	CTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCC	1369
Qy	1160	TGGTCCTGCTGCTGCTTGTCTCATCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACT	1219
Db	1370	TGGTCCTGCTGCTGCTTGTCTCATCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACT	1429
Qy	1220	CAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1430	CAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1489
Qy	1280	GCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCA	1339
Db	1490	GCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCA	1549

Qy	1340	CCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCA	1399
Db	1550	CCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCA	1609
Qy	1400	ATGGGACACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCA	1459
Db	1610	ATGGGACACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCA	1669
Qy	1460	CCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGC	1519
Db	1670	CCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGC	1729
Qy	1520	CCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGA	1579
Db	1730	CCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGA	1789
Qy	1580	TCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCT	1639
Db	1790	TCCCTAATACAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCT	1849
Qy	1640	ATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTC	1699
Db	1850	ATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG-----	1887
Qy	1700	AGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAG	1759
Db	1888	-----AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAG	1924
Qy	1760	TCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCA	1819
Db	1925	TCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCA	1984
Qy	1820	AAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCT	1879
Db	1985	AAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCT	2044
Qy	1880	CCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGG	1939
Db	2045	CCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGG	2104
Qy	1940	GCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGC	1999
Db	2105	GCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGC	2164
Qy	2000	TTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGC	2059
Db	2165	TTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGC	2224
Qy	2060	ATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGC	2119
Db	2225	ATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGC	2284
Qy	2120	TGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCA	2179
Db	2285	TGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCA	2344
Qy	2180	TCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCC	2239

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      |||
Db      2345 TCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGTCAGCTACCAGGAGATCC 2404
      |||
Qy      2240 CCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGC 2299
      |||
Db      2405 CCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGC 2464
      |||
Qy      2300 GTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCG 2359
      |||
Db      2465 GTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCG 2524
      |||
Qy      2360 ACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGC 2419
      |||
Db      2525 ACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGC 2584
      |||
Qy      2420 TGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCC 2479
      |||
Db      2585 TGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCC 2644
      |||
Qy      2480 CCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCG 2539
      |||
Db      2645 CCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCG 2704
      |||
Qy      2540 ACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCA 2599
      |||
Db      2705 ACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCA 2764
      |||
Qy      2600 AGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCA 2659
      |||
Db      2765 AGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCA 2824
      |||
Qy      2660 ACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCA 2719
      |||
Db      2825 ACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCA 2884
      |||
Qy      2720 CAGTGTCTGGAGGCTGAGTGCTGA 2742
      |||
Db      2885 CAGTGTCTGGAGGCTGAGTGCTGA 2907

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# RESULT 5

ABK15169

ID ABK15169 standard; DNA; 3580 BP.

XX

AC ABK15169;

XX

DT 23-APR-2002 (first entry)

XX

DE Human REPTR 1 cDNA sequence.

XX

KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;  
KW anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective;  
KW antiallergic; antibody; immunogen; endometriosis;  
KW gastrointestinal disorder; gastritis; oesophageal carcinoma;  
KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;  
KW endocrine disorder; hypothalamus disorder; Kallman's disease;  
KW autoimmune disease; inflammatory disease; infertility; receptor;



KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;  
KW osteoarthritis; diabetes mellitus; multiple sclerosis;  
KW systemic lupus erythematosus; cell proliferative disorder; cancer;  
KW developmental disorder; Duchenne muscular dystrophy; gene;  
KW Becker muscular dystrophy; neurological disorder; epilepsy;  
KW Alzheimer's disease; Huntington's disease; reproductive disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 4. .2532

FT /\*tag= a

FT /product= "REPTR1 protein"

XX

PN WO200198354-A2.

XX

PD 27-DEC-2001.

XX

PF 21-JUN-2001; 2001WO-US019942.

XX

PR 21-JUN-2000; 2000US-0214027P.

PR 25-AUG-2000; 2000US-0228045P.

PR 12-DEC-2000; 2000US-0255104P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;  
PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;  
PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;  
PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;

XX

DR WPI; 2002-090432/12.

DR P-PSDB; AAU17818.

XX

PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in  
PT the diagnosis, treatment and prevention of gastrointestinal (e.g.  
PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell  
PT proliferative (e.g. cancer) disorders.

XX

PS Claim 57; Page 142-143; 157pp; English.

XX

CC This invention relates to twelve human receptors cDNA sequences referred  
CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The  
CC proteins of the invention may have antiinflammatory, cytostatic,  
CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active  
CC general, anticonvulsant, nootropic, neuroprotective, antiallergic  
CC activities. The sequences of the invention may be used to produce REPTR  
CC agonists or antagonists, and the protein sequences may be used to raise  
CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and  
CC polypeptides of the invention are useful in the diagnosis, treatment and  
CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,  
CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine  
CC (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory  
CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,  
CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,  
CC systemic lupus erythematosus), cell proliferative (e.g. cancer),  
CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological

CC (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and  
CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other  
CC examples of each disorder are given in the specification. The present  
CC sequence represents the human REPTR1 cDNA sequence of the invention  
XX  
SQ Sequence 3580 BP; 670 A; 1233 C; 1025 G; 652 T; 0 U; 0 Other;

Query Match 85.6%; Score 2356; DB 6; Length 3580;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

Qy	43	GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	102
Db	1	GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	60
Qy	103	CTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC	162
Db	61	CTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC	120
Qy	163	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAG	222
Db	121	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAG	180
Qy	223	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG	282
Db	181	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG	240
Qy	283	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	342
Db	241	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	300
Qy	343	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTG	402
Db	301	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTG	360
Qy	403	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	462
Db	361	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	420
Qy	463	GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	522
Db	421	GCCTACATCCGCATAGCCATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	480
Qy	523	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCC	582
Db	481	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCC	540
Qy	583	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	642
Db	541	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	600
Qy	643	ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCTTGCTGACACGGCCAACCTAC	702
Db	601	ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCTTGCTGACACGGCCAACCTAC	660
Qy	703	ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTC	762

Db	661	ACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTTCATCGTC	720
Qy	763	TACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGG	822
Db	721	TACGTG-----	726
Qy	823	CGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCT	882
Db	727	-----	726
Qy	883	TTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGC	942
Db	727	-----GACGGC	732
Qy	943	AGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	1002
Db	733	AGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	792
Qy	1003	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGGCACTGACCTG	1062
Db	793	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGGCACTGACCTG	852
Qy	1063	GACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG	1122
Db	853	GACACCCGCAACTGTACCAGTGACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGTG	912
Qy	1123	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCCTGCTGCTGCTTGTCTC	1182
Db	913	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCCTGCTGCTGCTTGTCTC	972
Qy	1183	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1242
Db	973	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1032
Qy	1243	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1302
Db	1033	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1092
Qy	1303	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1362
Db	1093	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1152
Qy	1363	CGGCAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1422
Db	1153	CGGCAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1212
Qy	1423	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1482
Db	1213	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1272
Qy	1483	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1542
Db	1273	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1332
Qy	1543	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC	1602
Db	1333	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTC	1392

Qy	1603	CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1662
Db	1393	CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1452
Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1782
Db	1513	AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1572
Qy	1783	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1842
Db	1573	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1632
Qy	1843	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTG	1902
Db	1633	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTG	1692
Qy	1903	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1962
Db	1693	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1752
Qy	1963	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	2022
Db	1753	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	2142
Db	1873	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	1932
Qy	2143	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	2202
Db	1933	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2052
Qy	2263	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGAC	2322
Db	2053	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGAC	2112
Qy	2323	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2382
Db	2113	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2172
Qy	2383	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2232

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Qy      2443  GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTTCGGCAGAAGATA 2502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2233  GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTTCGGCAGAAGATA 2292

Qy      2503  ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2293  ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2352

Qy      2563  CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2353  CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2412

Qy      2623  CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2413  CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2472

Qy      2683  GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2473  GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2532

Qy      2743  GGCCGGCCAG 2752
          |||||||||
Db      2533  GGCCGGCCAG 2542

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RESULT 6

AAV52940

ID AAV52940 standard; cDNA; 3014 BP.

XX

AC AAV52940;

XX

DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Rat UNC-5 homologue unc5h-1 cDNA.

XX

KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;

KW diagnosis; therapy; ds.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..2697

FT /\*tag= a

XX

PN WO9837085-A1.

XX

PD 27-AUG-1998.

XX

PF 19-FEB-1998; 98WO-US003143.

XX

PR 19-FEB-1997; 97US-00808982.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;

XX

Qy	46	ATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	105
Db	1	ATGGCCGTCCGGCCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT	60
Qy	106	CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCG	165
Db	61	CGTGGTTCGGGTGCCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCGCGCCAGGTGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAGGTGTTTCGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTCGGGCTGGAG	360

Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCCTGGAGCAAGGCATTGTACTACCTTGTGCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACCTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACCTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGACGCGCTCCGCTGCTGTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200

[illegible]





XX  
 KW YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;  
 KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;  
 KW calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;  
 KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;  
 KW tumour necrosis factor alpha; TNF-alpha; rat.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .2697  
 FT /\*tag= a  
 FT /product= "Rat netrin receptor UNC5H1"  
 XX  
 PN WO200175440-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 02-APR-2001; 2001WO-GB001486.  
 XX  
 PR 31-MAR-2000; 2000GB-00007880.  
 PR 26-MAY-2000; 2000GB-00012768.  
 XX  
 PA (WELF-) WELFIDE CORP.  
 XX  
 PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;  
 XX  
 DR WPI; 2002-010813/01.  
 DR P-PSDB; AAU10543.  
 XX  
 PT Novel chronic animal model of schizophrenia, useful for identifying anti-  
 PT psychotic drugs and genes that are associated with schizophrenia.  
 XX  
 PS Claim 1; Fig 8a; 79pp; English.  
 XX  
 CC The invention relates to YSG polynucleotide fragments for use in  
 CC diagnosing and/or developing treatments for schizophrenia using chronic  
 CC animal models. The polynucleotides and their encoded polypeptides are  
 CC used for identification of compounds which modulate the expression of YSG  
 CC molecules, leading to the manufacture of schizophrenia medicaments. The  
 CC sequences can also be used for testing candidate compounds for any effect  
 CC on the polypeptides. Anti-schizophrenic effects of a compound can be  
 CC determined by measuring local cerebral glucose utilisation (LCGU) or  
 CC comparing its expression level with that of a control group. The  
 CC sequences are useful in the identification of genes associated with  
 CC schizophrenic states and in the development of an antibody. The sequences  
 CC of the invention include phosphodiesterase 1-alpha, calcium-independent  
 CC alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain  
 CC receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and  
 CC tumour necrosis factor (TNF) alpha. This sequence represents rat netrin  
 CC receptor UNC5H1 (YSG7) DNA  
 XX  
 SQ Sequence 2697 BP; 541 A; 864 C; 766 G; 526 T; 0 U; 0 Other;

Query Match 81.8%; Score 2252.2; DB 6; Length 2697;  
 Best Local Similarity 89.7%; Pred. No. 0;  
 Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Qy	46	ATGGCCGTC	CGGCCCGGCCTGTGGCCAGTCCTCTGGGCATAGTCCTCGCCGCTTGGCTC	105
Db	1	ATGGCCGTC	CGGCCCGGCCTGTGGCCAGTCCTCTGGGCATAGTCCTCGCCGCTTGGCTT	60
Qy	106	CGCGGCTCGGGT	GCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG	165
Db	61	CGTGGTTTCGGGT	GCCCAGCAGAGTGCCACCGTGGCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCC	ACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCC	ACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGT	GCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGT	GCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGT	TGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCC	345
Db	241	TGGGTCCGCCAGGT	CGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCG	CATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAG	405
Db	301	ACCATGGAGGTCCG	TATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTCGGGCTGGAG	360
Qy	406	GAATACTGGTGCC	AGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCC	AGTGCGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGC	CAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGC	CTATTTGCGCAAGAACTTCGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGG	CATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGG	CATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCG	GAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCG	AAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAG	CCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAATACTACACC	705
Db	601	ACGCGGGAGCACAG	CCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAATACTACACC	660
Qy	706	TGCGTGGCCAAGA	ACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTCTAC	765
Db	661	TGTGTGGCCAAGA	ACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720
Qy	766	GTGAACGGTGGGT	GGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGT	GGTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAAC	GAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAAC	GAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGGCGCCTTC	840

Qy	886	TGTGAGGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCACTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGTCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGTCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGTCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCTTGTCTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCTAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCAACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCAACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAATACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785

Db	1681	TGTGGGCCCCCAGGAGTCTCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGCAAGCTACTTGTGAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCACTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCTCATTCGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCTCATTCGGCAAAAGATCATC	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAACTT	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625



PT the biopharmaceutical industry.  
XX  
PS Claim 7; Page 17; 32pp; English.  
XX

CC This partial cDNA, termed unc5h-1, comprises a human homologue of  
CC Caenorhabditis elegans unc-5. unc5h-1 and unc5h-2 (see AAV52943) cDNAs  
CC were isolated from an embryonic brain cDNA library. The predicted  
CC proteins (see AAW78899 and AAW78901) show similarity with UNC-5. They are  
CC predicted to be involved in cell migration and axon guidance, and are  
CC characterised as receptor proteins for netrins. Gene expression is  
CC observed in regions where differentiating neurons are undergoing  
CC axogenesis. Rat unc5h-1 (see AAV52940) and unc5h-2 (see AAV52942) cDNAs  
CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly  
CC from transfected host cells by utilising these vertebrate UNC-5 nucleic  
CC acids. The invention also provides unc-5 hybridisation probes and  
CC primers, vertebrate UNC-5-specific binding agents such as specific  
CC antibodies, and methods of making and using the subject compositions in  
CC diagnosis (e.g. genetic hybridisation screens for vertebrate unc-5  
CC transcripts), therapy (e.g. gene therapy to modulate vertebrate unc-5  
CC gene expression) and in the biopharmaceutical industry (e.g. as  
CC immunogens, reagents for modulating cell guidance, reagents for screening  
CC chemical libraries for lead pharmacological agents, etc.). (Updated on 25  
CC -MAR-2003 to correct PI field.)

XX  
SQ Sequence 1787 BP; 349 A; 603 C; 491 G; 344 T; 0 U; 0 Other;

Query Match 56.8%; Score 1562.4; DB 2; Length 1787;  
Best Local Similarity 98.5%; Pred. No. 2.1e-292;  
Matches 1661; Conservative 0; Mismatches 16; Indels 9; Gaps 8;

Qy 1070 GCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCT 1129  
Db 1 GCAACTGTACCAGTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCT 59  
Qy 1130 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTTGTCTCATCCTCG 1189  
Db 60 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTTGTCTCATCCTCG 119  
Qy 1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249  
Db 120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179  
Qy 1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCATCTGCTCACC 1308  
Db 180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCATCTGCTCACC 239  
Qy 1309 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 1368  
Db 240 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 299  
Qy 1369 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 1428  
Db 300 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 359  
Qy 1429 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 1488  
Db 360 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 419

Smotrophin  
Domain

Qy	1489	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	1548
Db	420	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	479
Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
Db	480	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC	539
Qy	1609	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	1668
Db	540	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	599
Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	1728
Db	600	GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	GGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTT-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAG	2208
Db	1077	AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCAGCTCCCTGTGGAAG	1134
Qy	2209	AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAG	2268
Db	1135	AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	1254



Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	ATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
Db	1375	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568
Db	1435	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	1494
Qy	2569	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	2628
Db	1495	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	1554
Qy	2629	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	2688
Db	1555	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	1614
Qy	2689	GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC	2746
Db	1615	GGGACTGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTCGGAGGCTGAGTGCTGAGGCC	1674
Qy	2747	GGCCAG	2752
Db	1675	GGCCAG	1680

# RESULT 9

AAC90958

ID AAC90958 standard; cDNA; 9700 BP.

XX

AC AAC90958;

XX

DT 19-MAR-2001 (first entry)

XX

DE Plasmid pGC1037 nucleotide sequence SEQ ID NO:91.

XX

KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;

KW protein-protein interaction; identification; ss.

XX

OS Synthetic.

XX

PN WO200073328-A2.

XX

~~DD~~ 07-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-EP005108.

XX

PR 01-JUN-1999; 99GB-00012755.

XX

PA (DEVG-) DEVGEN NV.

*pre-APA*

XX  
 PI Van Crielinge W, Roelens I, Bogaert T, Verwaerde P;  
 XX  
 DR WPI; 2001-016508/02.  
 XX  
 PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a  
 PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for  
 PT identifying unknown human cDNAs which encode proteins that interact with  
 PT the human unc-5C protein.  
 XX  
 PS Example 4; Page 228-230; 246pp; English.  
 XX  
 CC The present invention describes 3 variants of human unc-5C cDNAs (unc-  
 CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-  
 CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the  
 CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on  
 CC protein-protein-interactions between the unc-5 protein and a variety of  
 CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1  
 CC cDNA are useful in methods for identifying compounds which reduce or  
 CC inhibit the lethal phenotype associated with the expression of the unc-5  
 CC death domain in yeast. They are also useful in yeast two hybrid  
 CC experiments for identifying unknown human cDNAs which encode proteins  
 CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and  
 CC AAB50646 to AAB50693 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 9700 BP; 2604 A; 2193 C; 2236 G; 2666 T; 0 U; 1 Other;

Query Match 47.4%; Score 1304.2; DB 4; Length 9700;  
 Best Local Similarity 99.8%; Pred. No. 2.1e-242;  
 Matches 1306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1437 CACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTTCGTCTCCCGCCTCTCCAC 1496  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 7 CACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTTCGTCTCCCGCCTCTCCAC 66  
 Qy 1497 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAACATGACCTATGGGACCTTCAA 1556  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 67 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAACATGACCTATGGGACCTTCAA 126  
 Qy 1557 CTTCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGA 1616  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 127 CTTCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCAGA 186  
 Qy 1617 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 1676  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 187 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 246  
 Qy 1677 GAGGTTGCCCCTAGCTGGCTGTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 1736  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 247 GAGGTTGCCCCTAGCTGGCTGTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 306  
 Qy 1737 TGGCGTCTGCTCACCCGGCCAGTCATCTGGCTATGGACCACTGTGGGGAGCCCAGCCC 1796  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 307 TGGCGTCTGCTCACCCGGCCAGTCATCTGGCTATGGACCACTGTGGGGAGCCCAGCCC 366  
 Qy 1797 TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT 1856

Db	367	 TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	426
Qy	1857	GCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG	1916
Db	427	 GCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG	486
Qy	1917	CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	1976
Db	487	 CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	546
Qy	1977	TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	2036
Db	547	 TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	606
Qy	2037	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	2096
Db	607	 CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	666
Qy	2097	GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAG	2156
Db	667	 GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAG	726
Qy	2157	TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT	2216
Db	727	 TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT	786
Qy	2217	CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	2276
Db	787	 CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	846
Qy	2277	GCACTGCACCTTCACCCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	2336
Db	847	 GCACTGCACCTTCACCCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	906
Qy	2337	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	2396
Db	907	 GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	966
Qy	2397	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT	2456
Db	967	 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCAAGCCCTGGT	1026
Qy	2457	GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	2516
Db	1027	 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	1086
Qy	2517	CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG	2576
Db	1087	 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG	1146
Qy	2577	CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA	2636
Db	1147	 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA	1206
Qy	2637	GGCGGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG	2696

Db 1207 GGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 1266

Qy 2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGC 2745

Db 1267 CCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGTC 1315

RESULT 10

AAH99530

ID AAH99530 standard; cDNA; 1321 BP.

XX

AC AAH99530;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein encoding cDNA sequence SEQ ID NO:365.

XX

KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;  
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200153455-A2.

XX

PD 26-JUL-2001.

XX

PF 22-DEC-2000; 2000WO-US035017.

XX

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457603/49.

DR P-PSDB; AAM25589.

XX

PT Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX

PS Claim 1; Page 471; 1217pp; English.

XX

CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 CC AAM25963. The proteins can have activities based on the tissues and cells  
 CC they are expressed in, such as: antiinflammatory; antirheumatic;  
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;  
 CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;  
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antisense therapy and vaccine  
 CC production, The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders

XX

SQ Sequence 1321 BP; 258 A; 440 C; 371 G; 252 T; 0 U; 0 Other;

Query Match 43.8%; Score 1206.6; DB 4; Length 1321;  
 Best Local Similarity 98.0%; Pred. No. 1.1e-223;  
 Matches 1295; Conservative 0; Mismatches 19; Indels 7; Gaps 7;

Qy	1435	CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC	1494
Db	1	CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC	60
Qy	1495	ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC	1554
Db	61	ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC	120
Qy	1555	AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCA	1614
Db	121	AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCA	180
Qy	1615	GATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC	1674
Db	181	GATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC	240
Qy	1675	GTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	1734
Db	241	GTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	300
Qy	1735	CCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-GGCTATGGACCACTGT-GGGGAGCCC	1791
Db	301	CCTGGGCGTCCTGCTTACCCGGCCAGTCATCCTGGGGTATGGACCACTGTGGGGGAGCCC	360
Qy	1792	AGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	1850
Db	361	AGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	420
Qy	1851	TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAG	1910

Db	421	TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	480
Qy	1911	TGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAG	1970
Db	481	TGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATGCCCTGGTGGGAGAGGCCCTCAG	540
Qy	1971	CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	2030
Db	541	CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	600
Qy	2031	CGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGT	2090
Db	601	CGAGTACAACATACTGGTCTACTGCCTGCATGACACTCACGATGCACTCAACGTAGTGGT	660
Qy	2091	GCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAA	2150
Db	661	GCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGGAGCCACTGGTACTGCACTTCAA	720
Qy	2151	GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	2210
Db	721	GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	780
Qy	2211	TAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG	2270
Db	781	TAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG	840
Qy	2271	GTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	2330
Db	841	GTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	900
Qy	2331	CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	2390
Db	901	CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	960
Qy	2391	CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	2450
Db	961	CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	1020
Qy	2451	CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG	2510
Db	1021	CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG	1080
Qy	2511	CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT	2570
Db	1081	CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT	1140
Qy	2571	GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT	2630
Db	1141	GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT	1200
Qy	2631	GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT-G	2689
Db	1201	GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGG	1260
Qy	2690	GACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCCG	2747

Db 1261 GACTGGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTCGGAGGCTGAGTGCTGAGGCCG 1320  
Qy 2748 G 2748  
|  
Db 1321 G 1321

RESULT 11

AAS75738

ID AAS75738 standard; cDNA; 3646 BP.

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AC AAS75738;

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DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #11542.

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KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

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OS Homo sapiens.

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PN WO200175067-A2.

XX

PD 11-OCT-2001.

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PF 30-MAR-2001; 2001WO-US008631.

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PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

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PA (HYSE-) HYSEQ INC.

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PI Drmanac RT, Liu C, Tang YT;

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DR WPI; 2001-639362/73.

DR P-PSDB; ABG11551.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

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PS Claim 1; SEQ ID NO 11542; 103pp; English.

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CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

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SQ Sequence 3646 BP; 930 A; 917 C; 921 G; 877 T; 0 U; 1 Other;

Query Match 35.2%; Score 970; DB 5; Length 3646;  
Best Local Similarity 61.3%; Pred. No. 6.6e-178;  
Matches 1680; Conservative 1; Mismatches 996; Indels 63; Gaps 5;

```
Qy      57  GCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGG 116
      || || || || || || || || || || || || || || || || || || || ||
Db      220  GCTCGTGCTACCTGCCCTGGCCCTGCTCAGCGCCAGCGGCACTGGCTCCGCCGCCCAAGA 279

Qy      117  TGCCACAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
      || || || || || || || || || || || || || || || || || || || ||
Db      280  TGATGACTTTTTTTCATGAACTCCAGAACTTTTCTTCTGATCCACCTGAGCCTCTGCC 339

Qy      177  CCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGT 236
      || || || || || || || || || || || || || || || || || || || ||
Db      340  ACATTTCTTTATTGAGCCTGAAGAAGCTTATATTGTGAAGAATAAGCCTGTGAACCTGTA 399

Qy      237  GTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCA 296
      || || || || || || || || || || || || || || || || || || || ||
Db      400  CTGTAAAGCAAGCCCTGCCACCCAGATCTATTTCAGTGTAATAGTGAATGGGTTCATCA 459

Qy      297  GGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGT 356
      | |||| || || || || || || || || || || || || || || || || || ||
Db      460  GAAGGACCACATAGTAGATGAAAGAGTAGATGAAACTTCCGGTCTCATTTGTCCGGGAAGT 519

Qy      357  CCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTGCGGCTGGAGGAATACTGGTG 416
      || || || || || || || || || || || || || || || || || || || ||
Db      520  GAGCATTGAGATTTCGCGCCAGCAAGTGAAGAACTCTTTGGACCTGAAGATTACTGGTG 579

Qy      417  CCAAGTGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCAT 476
      || || || || || || || || || || || || || || || || || || || ||
Db      580  CCAAGTGTGTGGCCTGGAGCTCCGCGGGTACCACAAAGAGCCGGAAGGCGTATGTGCGCAT 639

Qy      477  AGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCA 536
      || || || || || || || || || || || || || || || || || || || ||
Db      640  TGCATATCTACGGAAGACATTTGAGCAGGAACCCCTAGGAAAGGAAGTGTCTTTGGAACA 699

Qy      537  GGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCT 596
      || || || || || || || || || || || || || || || || || || || ||
Db      700  GGAAGTCTTACTCCAGTGTGACCACTGAAGGGATCCCAGTGGCTGAGGTGGAATGGTT 759

Qy      597  CCGGAACGAGGACCTGGTGGACCCGTCCTTGGACCCCAATGTATACATCACGCGGGAGCA 656
      || || || || || || || || || || || || || || || || || || || ||
Db      760  GAAAATGAAGACATAATTGATCCCGTTGAAGATCGGAATTTTATATTACTATTGATCA 819

Qy      657  CAGCCTGGTGGTGGCAGAGCCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAA 716
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Db 820 CAACCTCATCATAAAGCAGGCCCGACTCTCTGATACTGCAAATTACACCTGTGTTGCCAA 879  
 Qy 717 GAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCTACGTGAACGGTGG 776  
 Db 880 AAACATTGTTGCCAAGAGGAAAAGTACAACCTGCCACTGTCTAGTCTATGTCAACGGTGG 939  
 Qy 777 GTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAA 836  
 Db 940 CTGGTCCACCTGGACGGAGTGGTCTGTGTGTAACAGCCGCTGTGGACGAGGGTATCAGAA 999  
 Qy 837 ACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCA 896  
 Db 1000 ACGTACAAGGACTTGTACCAACCCGGCACCCTCAATGGGGGTGCCTTCTGTGAAGGGCA 1059  
 Qy 897 GAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTG 956  
 Db 1060 GAGTGTGCAGAAAATAGCCTGTACTACGTTATGCCAGTGGATGGCAGGTGGACGCCATG 1119  
 Qy 957 GAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGA 1016  
 Db 1120 GAGCAAGTGGTCTACTTGTGGAAGTGAAGTGCACCCACTGGCGCAGGAGGGAGTGCACGGC 1179  
 Qy 1017 CCCAGCACCCCGCAACGGAGGGGAGGAGTGCAGGGGCACTGACCTGGACACCCGCAACTG 1076  
 Db 1180 GCCAGCCCCCAAGAATGGAGGCAAGGACTGCGACGGCCTCGTCTTGCAATCCAAGAACTG 1239  
 Qy 1077 TACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGG 1136  
 Db 1240 CACTGATGGGCTTTGCATGCAGACTGCTCCTGATTGATGATGTTGCTCTCTATGTTGG 1299  
 Qy 1137 ---CCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCTCATCTCGTTTA 1193  
 Db 1300 GATTGTGATAGCAGTGATCGTTTGCCTGGCGATCTCTGTAGTTGTGGCCTTGTGTTGTA 1359  
 Qy 1194 TTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGG 1253  
 Db 1360 TCGGAAGAATCATCGTGACTTTGAGTCAGATATTATTGACTCTTCGGCACTCAATGGGGG 1419  
 Qy 1254 CTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCA 1313  
 Db 1420 CTTTCARCCTGTGAACATCAAG-----GCAGCAAGACAAGATCTGCTGGCTGTACC 1470  
 Qy 1314 GCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATG- 1372  
 Db 1471 CCCAGACCTCACGTGAGCTGCAGCCATGTACAGAGGACCTGTCTATGCCCTGCATGACGT 1530  
 Qy 1373 ----GGCCCAGCCCCAAGTTCAGCTCACCAT----GGGCACCTGCTCAGCCCCCTGGG 1424  
 Db 1531 CTCAGACAAAATCCCAATGACCAACTCTCCAATTCTGGATCCACTGCCCAACCTGAAAAT 1590  
 Qy 1425 TGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTC 1484  
 Db 1591 CAAAGTGTACAACACCTCAGGTGCTGTCTCCCCCAAGATGACCTCTCTGAGTTTACGTC 1650  
 Qy 1485 CCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGA---- 1540

Db 1651 CAAGCTGTCCCCTCAGATGACCCAGTCGTTGTTGGAGAATGAAGCCCTCAGCCTGAAGAA 1710

Qy 1541 -----CCTATGGGACCTTCAACTTCCT 1562  
| | | | | | | | | |

Db 1711 CCAGAGTCTAGCAAGGCAGACTGATCCATCCTGTACCGCATTTGGCAGCTTCAACTCGCT 1770

Qy 1563 CGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCAT 1622  
| | | | | | | | | | | | | | | | | | | |

Db 1771 GGGAGGTCACCTTATTGTTCCCAATTCAGGAGTCAGCTTGCTGATTCCCGCTGGGGCCAT 1830

Qy 1623 ACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTT 1682  
| | | | | | | | | | | | | | | | | | | |

Db 1831 TCCCCAAGGGAGAGTCTACGAAATGTATGTGACTGTACACAGGAAAGAACTATGAGGCC 1890

Qy 1683 GCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGT 1742  
| | | | | | | | | | | | | | | | | | | |

Db 1891 ACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGAGCTGTGGGGCCCCAGGAGC 1950

Qy 1743 CCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAG 1802  
| | | | | | | | | | | | | | | | | | | |

Db 1951 TCTGCTCACCCGCCCCGTCGTCCTCACTATGCATCACTGCGCAGACCCCCAATACCGAGGA 2010

Qy 1803 CTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCT 1862  
| | | | | | | | | | | | | | | | | | | |

Db 2011 CTGGAAAATACTGCTCAAGAACCAGGCAGCACAGGGACAGTGGGAGGATGTGGTGGTGGT 2070

Qy 1863 GGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGT 1922  
| | | | | | | | | | | | | | | | | | | |

Db 2071 CGGGGAGGAAAACCTTCAACCACCCCTGCTACATTAAGCTGGATGCAGAGGCCTGCCACAT 2130

Qy 1923 CTTCAACCGAGCAGCTGGGCGGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGC 1982  
| | | | | | | | | | | | | | | | | | | |

Db 2131 CCTCACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGCGGCTGC 2190

Qy 1983 CAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACAT 2042  
| | | | | | | | | | | | | | | | | | | |

Db 2191 AAAGCGCCTCAAGCTGGCCATCTTTGGGCCCTGTGCTGCTCCTCGCTGGAGTACAGCAT 2250

Qy 2043 CCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAA 2102  
| | | | | | | | | | | | | | | | | | | |

Db 2251 CCGAGTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAAATTTTACATCTTGAGAG 2310

Qy 2103 GCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTACCA 2162  
| | | | | | | | | | | | | | | | | | | |

Db 2311 ACAGACGGGAGGACAGCTCCTAGAAGAACCTAAGGCTCTTCATTTTAAAGGCAGACCCA 2370

Qy 2163 CAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGT 2222  
| | | | | | | | | | | | | | | | | | | |

Db 2371 CAACCTGCGCCTGTCAATTCAGATATCGCCCATTCCCTCTGGAAGAGCAAATTGCTGGC 2430

Qy 2223 CAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTG 2282  
| | | | | | | | | | | | | | | | | | | |

Db 2431 TAAATATCAGGAAATTCATTTTACCATGTTTGGAGTGGATCTCAAAGAAACCTGCACTG 2490

Qy 2283 CACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGT 2342  
| | | | | | | | | | | | | | | | | | | |

Db 2491 CACCTTCACTCTGGAAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAACCTCTGTGT 2550



PF 29-NOV-2001; 2001WO-US048922.

XX

PR 29-NOV-2000; 2000US-0253834P.

PR 30-NOV-2000; 2000US-0250926P.

PR 25-JAN-2001; 2001US-0264180P.

PR 20-AUG-2001; 2001US-0313656P.

PR 05-OCT-2001; 2001US-0327456P.

PR 28-NOV-2001; 2001US-00327456.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Edinger S, Macdougall JR, Millet I, Ellerman K, Stone DJ;  
PI Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CE;  
PI Casman SJ, Spytek KA, Boldog FL, Li L, Padigaru M, Mishra V;  
PI Patturajan M, Shenoy S, Rastelli L, Tchernev VT, Vernet CAM;  
PI Zerhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;

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DR WPI; 2002-590741/63.

DR P-PSDB; AA018734.

XX

PT Novel isolated polypeptide, designated NOVX, useful for treating or  
PT preventing in NOVX-associated disorders e.g. cardiomyopathy,  
PT atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.

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PS Claim 9; Page 11; 353pp; English.

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CC The present invention provides the protein and coding sequences of  
CC several novel human proteins, designated NOVX. These can be used in the  
CC treatment of, amongst others, cancers, autoimmune diseases, infections,  
CC inflammatory diseases, storage disorders, muscle disorders,  
CC neurodegenerative diseases and developmental defects. The present  
CC sequence is a coding sequence of the invention

XX

SQ Sequence 2860 BP; 555 A; 950 C; 860 G; 495 T; 0 U; 0 Other;

Query Match 34.0%; Score 936.2; DB 6; Length 2860;  
Best Local Similarity 61.7%; Pred. No. 2.2e-171;  
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

Qy 143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202  
|| | | | | | | | | | | | | | | | | | | | | | |  
Db 168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227  
  
Qy 203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262  
| | | | | | | | | | | | | | | | | | | | | |  
Db 228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA 287  
  
Qy 263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322  
| | | | | | | | | | | | | | | | | | | | | |  
Db 288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347  
  
Qy 323 CAGACGGGAGCAGTGGGCTGCCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382  
| | | | | | | | | | | | | | | | | | | | | |  
Db 348 TGGATGAGGCCACCGGTCTGCGGGTGC GCGAGGTGCAGATCGAGGTGTGCGGGCAGCAGG 407  
  
Qy 383 TCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442  
| | | | | | | | | | | | | | | | | | | | | |

Db 408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG 467  
 QY 443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
 ||||| ||||| ||||| ||| ||||| ||||| |||||  
 Db 468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527  
 QY 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 528 AGGAGCCTCTGGGCAAGGAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCCG 587  
 QY 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 588 CGGAGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647  
 QY 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCC 682  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 707  
 QY 683 TTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742  
 | | ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 708 TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAACGCCGGAGCA 767  
 QY 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 || | || | ||||| ||||| ||||| ||||| ||||| |||||  
 Db 768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827  
 QY 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 |||| | | ||||| ||||| ||||| ||||| ||||| |||||  
 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGACCTGCACCAACCCCG 887  
 QY 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | || ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 888 CTCCACTCAACGAGGGGCCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 947  
 QY 923 CCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGG 982  
 || | ||||| || || ||||| ||||| ||||| ||||| |||||  
 Db 948 CCATCTGCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTTCAGCTGCAGCACTG 1007  
 QY 983 ACTGCACCCACTGGCGGAGCCGTGAGTGTCTGACCCAGCACCCGCAACGGAGGGGAGG 1042  
 | || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067  
 QY 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | || | || || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127  
 QY 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | | ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTTCGTGG 1187  
 QY 1163 TCCTGCTGCTGCTTGTCTCATCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG 1222  
 | || || || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247  
 QY 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
 | | ||||| || ||||| ||||| ||||| ||||| |||||  
 Db 1248 ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307

Qy 1280 GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1308 CAAGGCCCAGTAACCCGAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367

Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA----- 1370  
 || || | | | | | | | | | | | | | | | | | |  
 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427

Qy 1371 -----TGGGCCCCAGCCCCAAGTTCCAGCTCACCA----- 1399  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1428 CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487

Qy 1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547

Qy 1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACT 1507  
 || | | | | | | | | | | | | | | | | | | | | | |  
 Db 1548 GCACATACCCTAGCGATTTCGCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607

Qy 1508 TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT 1552  
 || | | | | | | | | | | | | | | | | | | | | | |  
 Db 1608 TCGGTTCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667

Qy 1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC 1612  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA 1727

Qy 1613 CAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787

Qy 1673 ACGTGAGGTTGCCCCTAGCTGGCTGTGACCCCTGCTGAGTCCCATCGTTAGCTGTGGAC 1732  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1788 GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGAC 1847

Qy 1733 CCCCTGGCGTCTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA 1792  
 || | | | | | | | | | | | | | | | | | | | | | |  
 Db 1848 CCACAGGCCTCCTGCTGTGCCGCCCGGTGATCCTCACCATGCCCCACTGTGCCGAAGTCA 1907

Qy 1793 GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG 1852  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1908 GTGCCCCTGACTGGATCTTTCAGCTCAAGACCCAGGCCCACCAGGGCCACTGGGAGGAGG 1967

Qy 1853 TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG 1912  
 || || | | | | | | | | | | | | | | | | | | | | | |  
 Db 1968 TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG 2027

Qy 1913 CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG 1972  
 |||| | | | | | | | | | | | | | | | | | | | | | |  
 Db 2028 CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCTATTCCC 2087

Qy 1973 TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG 2032  
 | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG 2147



DE Human NOV1b coding sequence.

XX

KW Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;  
KW storage disorder; muscle disorder; neurodegenerative disorder; nootropic;  
KW developmental defect; neuroprotective; antiparkinsonian; hypotensive;  
KW hypertensive; haemostatic; cardiant; antianginal; dermatological;  
KW immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;  
KW antiparasitic; antiallergic; antiasthmatic; antirheumatic; antiarthritic;  
KW vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic;  
KW nephrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant;  
KW antiinfertility; antimanic; antidepressant; metabolic; cytostatic;  
KW tranquilizer; analgesic; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200257450-A2.

XX

PD 25-JUL-2002.

XX

PF 29-NOV-2001; 2001WO-US048922.

XX

PR 29-NOV-2000; 2000US-0253834P.  
PR 30-NOV-2000; 2000US-0250926P.  
PR 25-JAN-2001; 2001US-0264180P.  
PR 20-AUG-2001; 2001US-0313656P.  
PR 05-OCT-2001; 2001US-0327456P.  
PR 28-NOV-2001; 2001US-00327456.

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PI Edinger S, Macdougall JR, Millet I, Ellerman K, Stone DJ;  
PI Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CE;  
PI Casman SJ, Spytek KA, Boldog FL, Li L, Padigaru M, Mishra V;  
PI Patturajan M, Shenoy S, Rastelli L, Tchernev VT, Vernet CAM;  
PI Zerhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;

XX

DR WPI; 2002-590741/63.  
DR P-PSDB; AAO18735.

XX

PT Novel isolated polypeptide, designated NOVX, useful for treating or  
PT preventing in NOVX-associated disorders e.g. cardiomyopathy,  
PT atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.

XX

PS Claim 9; Page 14; 353pp; English.

XX

CC The present invention provides the protein and coding sequences of  
CC several novel human proteins, designated NOVX. These can be used in the  
CC treatment of, amongst others, cancers, autoimmune diseases, infections,  
CC inflammatory diseases, storage disorders, muscle disorders,  
CC neurodegenerative diseases and developmental defects. The present  
CC sequence is a coding sequence of the invention

XX

SQ Sequence 2860 BP; 557 A; 950 C; 858 G; 495 T; 0 U; 0 Other;

Query Match 34.0%; Score 936.2; DB 6; Length 2860;  
Best Local Similarity 61.7%; Pred. No. 2.2e-171;  
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;



Qy	143	ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATG	202
Db	168	ACTCCTTCCCCTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG	227
Qy	203	TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA	262
Db	228	CCTACATTGTGAAGAACAAGCCTGTGGAGCTTCGCTGCCGCGCCTTCCCCGCCACACAGA	287
Qy	263	TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA	322
Db	288	TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC	347
Qy	323	CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG	382
Db	348	TGGATGAGGCCACCGGCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTGCGGGCAGCAGG	407
Qy	383	TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG	442
Db	408	TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAG	467
Qy	443	GCACCACCAAGAGTCAGAAGGCCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC	502
Db	468	GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC	527
Qy	503	AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC	562
Db	528	AGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCCG	587
Qy	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622
Db	588	CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAAATGAGGATGTCATCGACCCCA	647
Qy	623	CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC	682
Db	648	CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC	707
Qy	683	TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCG	742
Db	708	TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGAGCA	767
Qy	743	CCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG	802
Db	768	CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC	827
Qy	803	TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG	862
Db	828	CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG	887
Qy	863	CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA	922
Db	888	CTCCACTCAACGAGGGGCCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCTGCACCA	947
Qy	923	CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGG	982
Db	948	CCATCTGCCCAGTCGATGGGGCGTGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG	1007

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1008 AGTGTGCCCCTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCACTGACCTCTGTGTACACAGTG 1102  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127

Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGTGG 1187

Qy 1163 TCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG 1222  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247

Qy 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1248 ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307

Qy 1280 GCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1308 CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367

Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA----- 1370  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427

Qy 1371 -----TGGGCCCAGCCCCAAGTTCAGCTCACCA----- 1399  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1428 CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487

Qy 1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547

Qy 1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTTCGTCTCCCGCCTCTCCACCCAGAACTACT 1507  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1548 GCACATACCCTAGCGATTTTCGCCCCGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607

Qy 1508 TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT 1552  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1608 TCGGTTCCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667

Qy 1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC 1612  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA 1727

Qy 1613 CAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787

Qy 1673 ACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTCCCATCGTTAGCTGTGGAC 1732  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1788 GTACCCTGCCGCTTTCAGAAAGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGAC 1847

Qy 1733 CCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA 1792

Db	1848 CCACAGGCCTCCTGCTGTGCCGCCCCGTATCCTCACCATGCCCCACTGTGCCGAAGTCA	1907
Qy	1793 GCCCTGACAGCTGGAGCCTGCGCCTCAA <sup>AAAA</sup> AAGCAGTCGTGCGAGGGCAGCTGGGAGGATG	1852
Db	1908 GTGCCCCTGACTGGATCTTTTCAGCTCAAGACCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853 TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968 TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG	2027
Qy	1913 CCTGCTACGTCTTCACCGAGCAGCTGGGCGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028 CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCTATTCCC	2087
Qy	1973 TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032
Db	2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033 AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC	2092
Db	2148 AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093 AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTTCAAGG	2152
Db	2208 AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153 ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268 ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTTGGAGGAGCA	2327
Qy	2213 AGCTCCTTGTGCTAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGT	2272
Db	2328 AGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273 ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388 CCCTCCA CTGCACTTTTACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333 AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTT CAGCATCAACTTCAACATCA	2392
Db	2448 AGATCTGCGTGC GGCAAGT GGAAGGGGAGGGCCAGATATTCAGCTGCATACCACTCTGG	2507
Qy	2393 CCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAG	2449
Db	2508 CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCTGGCAGCACTGTCACCA	2567
Qy	2450 CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTC CA	2509
Db	2568 CCCAGCTGGGACCTTATGCCTTCAAGATCCCCTGTCCATCCGCCAGAAGATATGCAACA	2627
Qy	2510 GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCAGAACTCCACC	2569
Db	2628 GCCTAGATGCCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA	2687
Qy	2570 TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC	2629



XX  
PF 07-JAN-2002; 2002WO-US000375.

XX  
PR 05-JAN-2001; 2001US-0260018P.  
PR 08-JAN-2001; 2001US-0260360P.  
PR 28-FEB-2001; 2001US-0272411P.  
PR 02-MAR-2001; 2001US-0272817P.  
PR 05-JUL-2001; 2001US-0303231P.  
PR 12-JUL-2001; 2001US-0305060P.  
PR 10-SEP-2001; 2001US-0318405P.  
PR 12-SEP-2001; 2001US-0318700P.  
PR 04-JAN-2002; 2002US-00037417.

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PA (CURA-) CURAGEN CORP.

XX  
PI Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;  
PI Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;  
PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;  
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;  
PI Padigar M, Taupier RJ, Miller CE, Eisen A;

XX  
DR WPI; 2002-583619/62.  
DR P-PSDB; ABB09520.

XX  
PT Novel polypeptides and nucleic acids homologous to transmembrane  
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
PT treating cancer, atherosclerosis, neurological, skin and autoimmune  
PT disorders.

XX  
PS Claim 9a; Page 121; 323pp; English.

XX  
CC The invention relates to 24 novel human proteins designated NOV1-NOV14  
CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and  
CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and  
CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-  
CC associated disorders or in the manufacture of a medicament for treating  
CC such disorders, with specific applications described for each of the 24  
CC NOVX proteins, based on their homology to known proteins. Various  
CC disorders are associated with NOVX proteins including neurological  
CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),  
CC pain, behavioural disorders, addiction, tuberous sclerosis, cancers  
CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders  
CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,  
CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease  
CC (e.g., hypertension), reproductive disorders, endometriosis,  
CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,  
CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine  
CC disorders, obesity, bacterial infections and particularly cardiomyopathy,  
CC atherosclerosis, cell signal processing-related disorders and disorders  
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may  
CC be used to identify cellular receptors or downstream effectors which  
CC binds to a NOVX protein, and are also useful as targets for the  
CC identification of small molecules that modulate or inhibit processes such  
CC as neurogenesis, cell differentiation, cell motility, cellular  
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX  
CC nucleic acid sequences can be used to identify a cell or tissue type and  
CC are useful as a source of primers or probes for forensic biology and for

CC identifying and cloning NOVX homologues in other cell types. Cells  
 CC comprising NOVX nucleic acids are useful for producing non-human  
 CC transgenic animals which are useful for studying the function and  
 CC activity of NOVX proteins and for identifying and evaluating modulators  
 CC of NOVX activity. The present sequence represents DNA encoding the  
 CC transmembrane receptor UNC5H2-like protein NOV11. The gene encoding NOV11  
 CC is located on chromosome 10

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SQ Sequence 2895 BP; 557 A; 960 C; 854 G; 524 T; 0 U; 0 Other;

Query Match 33.2%; Score 913.6; DB 6; Length 2895;  
 Best Local Similarity 61.6%; Pred. No. 5.1e-167;  
 Matches 1684; Conservative 0; Mismatches 919; Indels 129; Gaps 9;

Qy	143	ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATG	202
Db	140	ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG	199
Qy	203	TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA	262
Db	200	CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCGCCACACAGA	259
Qy	263	TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA	322
Db	260	TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC	319
Qy	323	CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG	382
Db	320	TGGATGAGGCCACCGGTCTGCGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG	379
Qy	383	TCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG	442
Db	380	TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG	439
Qy	443	GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC	502
Db	440	GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTGTCTGCGCAAGAACTTCGATC	499
Qy	503	AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC	562
Db	500	AGGAGCCTCTGGGCAAGGAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC	559
Qy	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622
Db	560	CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA	619
Qy	623	CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCAGACAGGCCCGCC	682
Db	620	CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCGCCAGGCCCGCC	679
Qy	683	TTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG	742
Db	680	TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAACGCCGAGCA	739
Qy	743	CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG	802
Db	740	CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC	799

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 800 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 859

Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | | | ||||| | | | |||| | |||| | | | |||| | | ||||| | |  
 Db 860 CTCCACTCAACGGAGGGGCGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 919

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGG 982  
 || | ||||| | | | |||| | ||||| | |||| | |||| | | |  
 Db 920 CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 979

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | | | ||||| | |||| | |||| | | | |||| | ||||| | ||||| |  
 Db 980 AGTGTGCCCAGTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1039

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | ||| | | | | | |||| | |||| | | | |||| | | | |||| |  
 Db 1040 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAGTG 1099

Qy 1103 CTTC-----TGGCCCTGAGGACGTGGCCCTCT 1129  
 || | | | |||| | |||| | |  
 Db 1100 AGTCACAGTGTGGTCCTCCTGTCCCCGCACTGCTGGAGGCCCTAGGGGATGCGGCGCTGT 1159

Qy 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGTGCTTGTCTCATCC 1186  
 ||| ||| ||| | ||| | ||| | ||| | || | || | || |  
 Db 1160 ATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCGTGGCAATCCTCATGGCGGTGGGGGTGG 1219

Qy 1187 TCGTTTATTGCCGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C 1243  
 | | | ||| | | | | |||| | | ||||| | | ||||| | |  
 Db 1220 TGGTGTACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCC 1279

Qy 1244 TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGC 1303  
 | | | ||||| ||||| | |||| | | | | | |||| | | |||| |  
 Db 1280 TGA CTGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGTAACCCGAGCTCC 1339

Qy 1304 T-----CACCATCCAGCCGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCT 1357  
 | | | | | | |||| | |||| | | |||| | | |||| | |  
 Db 1340 TACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCGCCGGCATCTACCGCGGACCCGTGT 1399

Qy 1358 GTCCCCGGCAGGA-----TG 1372  
 | ||| |||||  
 Db 1400 ATGCCCTGCAGGACTCCACCGACAAAATCCCCATGACCAACTCTCCTCTGCTGGACCCCT 1459

Qy 1373 GGCCAGCCCCAAGTTCCAGCTCACCA-----ATGGGCACCTGCTCAGCCCCCT 1421  
 ||||| ||| || || || || | |||| | | |||| |  
 Db 1460 TACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGGGCCAGGCCTGG 1519

Qy 1422 GGGTGGCGGCCGCCACAC-----ACTGCACCACAGCTCTCCACCTCTGAGGCCG 1471  
 | | |||| | | | |||| | | | |||| | | |||| |  
 Db 1520 CAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCTGGCACATACCCTAGCGATTTCGCCC 1579

Qy 1472 AGGAGTTCGTCTCCCGCTCTCCACCCAGAATACTTCCGCTC-----CC 1516  
 ||| | |||| | | | | | |||| | | |||| |  
 Db 1580 GGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCCTCGGTGCCAGCAGCTCTTGGGCC 1639

Qy 1517 TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA 1576  
 ||||| | | | | | | | | | | | | | | | | | | | | |  
 Db 1640 TGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCA 1699  
 Qy 1577 TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGA 1636  
 ||||| | | | | | | | | | | | | | | | | | | | | |  
 Db 1700 GCATCCCCGGCACAGGTGTGAGCTTGCTGGTGCCCAATGGAGCCATTCGCCAGGGCAAGT 1759  
 Qy 1637 TCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCCTAGCTGGCT 1696  
 |||| | | | | | | | | | | | | | | | | | | | | | |  
 Db 1760 TCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTGCCGCTTTTCAAGGGA 1819  
 Qy 1697 GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACC CGGC 1756  
 ||||| | | | | | | | | | | | | | | | | | | | | |  
 Db 1820 CCCAGACAGTATTGAGCCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCC 1879  
 Qy 1757 CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCCGCC 1816  
 | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1880 CCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCAGC 1939  
 Qy 1817 TCAAAAAGCAGTCGTGCGAGGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC 1876  
 |||| | | | | | | | | | | | | | | | | | | | | | |  
 Db 1940 TCAAGACCCAGGCCCACCAGGGCCACTGGGAGGAGGTGGTGACCCTGGATGAGGAGACCC 1999  
 Qy 1877 CCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCCTGCTACGTCTTCACCGAGCAGC 1936  
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 Db 2000 TGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTACATCCTGCTGGACCAGC 2059  
 Qy 1937 TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC 1996  
 |||| | | | | | | | | | | | | | | | | | | | | | |  
 Db 2060 TGGGCACCTACGTGTTACGGGCGAGTCTATTCCCGCTCAGCAGTCAAGCGGCTCCAGC 2119  
 Qy 1997 TGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCC 2056  
 || | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2120 TGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCC 2179  
 Qy 2057 TGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAC 2116  
 || | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2180 TGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGAT 2239  
 Qy 2117 AGCTGATCCAGGAGCCACGGGTCTTGCACTTCAAGGACAGTTACCACAACCTGCGCCTAT 2176  
 | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2240 ACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCT 2299  
 Qy 2177 CCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGA 2236  
 || | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2300 CCCTCCATGACCTCCCCCATGCCCATTGGAGGAGCAAGCTGCTGGCCAAATACCAGGAGA 2359  
 Qy 2237 TCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGG 2296  
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 Db 2360 TCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCACTTTTACCCTGG 2419  
 Qy 2297 AGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGG 2356  
 || | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2420 AGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAGTGGAAG 2479  
 Qy 2357 GCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG---GACACAAGGTTTGCTG 2413



Db	2480	GGGAGGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGG	2539
Qy	2414	AGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCA	2473
Db	2540	ACACTCTCTGCTCTGCCCCCTGGCAGCACTGTCAACACCCAGCTGGGACCTTATGCCTTCA	2599
Qy	2474	AGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGG	2533
Db	2600	AGATCCCCTGTCCATCCGCCAGAAGATATGCAACAGCCTAGATGCCCCCAACTCACGGG	2659
Qy	2534	GTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTG	2593
Db	2660	GCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCTGAATTACTTTG	2719
Qy	2594	CCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCA	2653
Db	2720	CCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACG	2779
Qy	2654	ACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCC	2713
Db	2780	ATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGG	2839
Qy	2714	TCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGC	2745
Db	2840	TGGCTGTGGCCACCGACGGGGACTGCTGAGCC	2871

# RESULT 15

AAS21316

ID AAS21316 standard; cDNA; 3884 BP.

XX

AC AAS21316;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA sequence encoding for PRO4326 polypeptide.

XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIA; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200140466-A2.

XX

PD 07-JUN-2001.

XX

PF 01-DEC-2000; 2000WO-US032678.

XX

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 09-DEC-1999; 99US-0170262P.

PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-408281/43.

DR P-PSDB; AAU12244.

XX

PT Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.

XX

PS Claim 3; Fig 145; 813pp; English.

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CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some

CC of the 275 sequences are also useful to stimulate the release of tumour  
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
 CC differentiation of chondrocytes, the proliferation or gene expression in  
 CC pericyte cells, the release of proteoglycans from cartilage, the  
 CC proliferation of inner ear utricular supporting cells or of T-  
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
 CC involved in binding interactions. The polynucleotides encoding PRO  
 CC polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy

XX

SQ Sequence 3884 BP; 767 A; 1278 C; 1162 G; 677 T; 0 U; 0 Other;

Query Match 32.8%; Score 902.4; DB 4; Length 3884;  
 Best Local Similarity 61.4%; Pred. No. 7.7e-165;  
 Matches 1677; Conservative 0; Mismatches 926; Indels 129; Gaps 9;

Qy	143	ACCCAGTGCCTGGTGCCAAACCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG	202
Db	507	ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG	566
Qy	203	TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGA	262
Db	567	CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA	626
Qy	263	TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA	322
Db	627	TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC	686
Qy	323	CAGACGGGAGCAGTGGGCTGCCACCATTGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG	382
Db	687	TGGATGAGGCCACCGGCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG	746
Qy	383	TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG	442
Db	747	TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAG	806
Qy	443	GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC	502
Db	807	GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC	866
Qy	503	AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC	562
Db	867	AGGAGCCTCTGGGCAAGGAGGTGCCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC	926
Qy	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622
Db	927	CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA	986
Qy	623	CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC	682
Db	987	CCCAGGACACCAACTTCTGCTCACCATCGACCACAACCTCATCATCGCCAGGCCCGCC	1046
Qy	683	TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG	742

Db 1047 TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 1106  
 QY 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCG 802  
 Db 1107 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 1166  
 QY 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 Db 1167 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 1226  
 QY 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 Db 1227 CTCCACTCAACGGAGGGGCGCTTCTGCGAGGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 1286  
 QY 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGG 982  
 Db 1287 CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1346  
 QY 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 Db 1347 AGTGTGCCCAGTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1406  
 QY 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGT- 1101  
 Db 1407 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATA 1466  
 QY 1102 -----GCTTCTGGCCCTGAGGACGTGGCCCTCT 1129  
 Db 1467 AGAAACTCTAAGCGACCCCAACAGCCACCTGCTGGAGGCCTCAGGGGATGCGGCGCTGT 1526  
 QY 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCC 1186  
 Db 1527 ATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGGCAATCCTCATGGCGGTGGGGGTGG 1586  
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 QY 1244 TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGC 1303  
 Db 1647 TGA CTGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGCAACCCGAGCTCC 1706  
 QY 1304 T-----CACCATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCT 1357  
 Db 1707 TACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCGCCGGCATCTACCGCGGACCCGTGT 1766  
 QY 1358 GTCCCCGGCAGGA-----TG 1372  
 Db 1767 ATGCCCTGCAGGACTCCACCGACAAAATCCCCATGACCAACTCTCCTCTGCTGGACCCCT 1826  
 QY 1373 GGCCAGCCCCAAGTTCCAGCTCACCA-----ATGGGCACCTGCTCAGCCCCCT 1421  
 Db 1827 TACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGGGCCAGGCCTGG 1886  
 QY 1422 GGGTGGCGGCCGCCACAC-----ACTGCACCACAGCTCTCCACCTCTGAGGCCG 1471

Db 1887 CAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTGGCACATACCCTAGCGATTTGCCCC 1946  
 Qy 1472 AGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTC-----CC 1516  
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 Db 1947 GGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCCTCGGTTCCCAGCAGCTCTTGGGCC 2006  
 Qy 1517 TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA 1576  
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 Db 2007 TGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCA 2066  
 Qy 1577 TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGA 1636  
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 Db 2067 GCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCAATGGAGCCATTCCCCAGGGCAAGT 2126  
 Qy 1637 TCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCT 1696  
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 Db 2127 TCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTCCCGCTTTTCAAGGGA 2186  
 Qy 1697 GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGC 1756  
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 Db 2187 CCCAGACAGTATTGAGCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCC 2246  
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 Qy 1817 TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC 1876  
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 Db 2307 TCAAGACCCAGGCCCACCAGGGCCACTGGGAGGAGGTGGTGACCCTGGATGAGGAGACCC 2366  
 Qy 1877 CCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGC 1936  
 | | | ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2367 TGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTCACATCCTGCTGGACCAGC 2426  
 Qy 1937 TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC 1996  
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 Db 2427 TGGGCACCTACGTGTTACGGGCGAGTCCTATTCCCGCTCAGCAGTCAAGCGGCTCCAGC 2486  
 Qy 1997 TGCTTCTGTTTTCGCCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCC 2056  
 || | || | || | | ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2487 TGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCC 2546  
 Qy 2057 TGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAC 2116  
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 Db 2547 TGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGAT 2606  
 Qy 2117 AGCTGATCCAGGAGCCACGGGTCTTCAAGGACAGTTACCACAACCTGCGCCTAT 2176  
 | || | ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2607 ACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCT 2666  
 Qy 2177 CCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGA 2236  
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 Db 2667 CCCTCCATGACCTCCCCCATGCCCATGGAGGAGCAAGCTGCTGGCCAAATACCAGGAGA 2726  
 Qy 2237 TCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGG 2296  
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 Db 2727 TCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCACTTTCACCCTGG 2786



OM nucleic - nucleic search, using sw model

Run on: July 12, 2004, 14:46:07 ; Search time 191 Seconds  
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 7995.942 Million cell updates/sec

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 Perfect score: 2752  
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
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 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2259	82.1	3014	2	US-08-808-982-1	Sequence 1, Appli
2	2259	82.1	3014	3	US-09-306-902A-1	Sequence 1, Appli
3	1562.4	56.8	1787	2	US-08-808-982-2	Sequence 2, Appli
4	1562.4	56.8	1787	3	US-09-306-902A-2	Sequence 2, Appli
5	1155.8	42.0	1282	4	US-09-833-381-1806	Sequence 1806, Ap
6	841.4	30.6	2831	2	US-08-808-982-3	Sequence 3, Appli
7	841.4	30.6	2831	3	US-09-306-902A-3	Sequence 3, Appli
8	432	15.7	1605	4	US-09-833-381-1807	Sequence 1807, Ap
c 9	269	9.8	771	1	US-08-253-155A-17	Sequence 17, Appl
10	119	4.3	305	2	US-08-808-982-4	Sequence 4, Appli
11	119	4.3	305	3	US-09-306-902A-4	Sequence 4, Appli

	12	53.6	1.9	657	3	US-08-985-526-2	Sequence 2, Appli
	13	53.6	1.9	1326	3	US-08-985-526-4	Sequence 4, Appli
	14	52.8	1.9	699	4	US-09-252-991A-7947	Sequence 7947, Ap
	15	52.8	1.9	1302	4	US-09-252-991A-7809	Sequence 7809, Ap
c	16	52.8	1.9	1947	4	US-09-252-991A-7533	Sequence 7533, Ap
	17	52.4	1.9	1770	4	US-09-252-991A-12265	Sequence 12265, A
	18	52.4	1.9	4884	4	US-09-252-991A-12126	Sequence 12126, A
c	19	52.4	1.9	4884	4	US-09-252-991A-12292	Sequence 12292, A
	20	52	1.9	7231	4	US-09-919-172-64	Sequence 64, Appl
	21	50.8	1.8	3885	4	US-09-369-364A-16	Sequence 16, Appl
	22	48.8	1.8	2493	4	US-09-252-991A-11987	Sequence 11987, A
c	23	48.8	1.8	2991	4	US-09-252-991A-12025	Sequence 12025, A
c	24	48.6	1.8	1068	4	US-09-252-991A-9933	Sequence 9933, Ap
	25	48.6	1.8	1251	4	US-09-252-991A-10142	Sequence 10142, A
	26	48.4	1.8	925	3	US-08-858-003-1	Sequence 1, Appli
	27	48.4	1.8	925	3	US-09-078-166-1	Sequence 1, Appli
	28	48.4	1.8	925	3	US-08-997-467-1	Sequence 1, Appli
	29	48.2	1.8	1288	1	US-08-440-856A-9	Sequence 9, Appli
	30	48.2	1.8	2034	4	US-09-252-991A-11958	Sequence 11958, A
c	31	48	1.7	8312	4	US-09-620-312D-1048	Sequence 1048, Ap
	32	47.8	1.7	2469	4	US-09-252-991A-5349	Sequence 5349, Ap
c	33	47.8	1.7	5103	4	US-09-252-991A-5192	Sequence 5192, Ap
	34	47.8	1.7	6876	4	US-09-252-991A-5283	Sequence 5283, Ap
	35	47.6	1.7	4257	2	US-08-690-473-1	Sequence 1, Appli
	36	47.6	1.7	4257	3	US-09-259-821A-1	Sequence 1, Appli
	37	47.6	1.7	4257	3	US-08-843-659-1	Sequence 1, Appli
	38	47	1.7	7218	1	US-08-232-463-14	Sequence 14, Appl
	39	46.2	1.7	1707	4	US-09-252-991A-10297	Sequence 10297, A
c	40	46.2	1.7	2511	4	US-09-252-991A-10560	Sequence 10560, A
	41	45.6	1.7	1627	4	US-09-675-018B-11	Sequence 11, Appl
	42	45.2	1.6	987	4	US-09-252-991A-7285	Sequence 7285, Ap
	43	45.2	1.6	1368	4	US-09-252-991A-7174	Sequence 7174, Ap
c	44	45.2	1.6	1575	4	US-09-252-991A-7330	Sequence 7330, Ap
	45	45	1.6	486	4	US-09-252-991A-8335	Sequence 8335, Ap

#### ALIGNMENTS

#### RESULT 1

US-08-808-982-1

; Sequence 1, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA



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;      ZIP: 94104
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/808,982
;      FILING DATE:
;      CLASSIFICATION: 530
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 3014 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
US-08-808-982-1

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Query Match          82.1%;  Score 2259;  DB 2;  Length 3014;
Best Local Similarity 89.7%;  Pred. No. 0;
Matches 2427;  Conservative 0;  Mismatches 280;  Indels 0;  Gaps 0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
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Db      1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT 60

Qy     106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
         || || ||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGTGGTTGCGGGTGCCCAGCAGAGTGCCACCGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
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Db     121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
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Db     181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
         ||||| |||||||| || ||||| || || |||||||| ||| ||||| || ||||
Db     241 TGGGTCCGCCAGGTGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTGCGGCTGGAG 405
         |||||||||||||| || || || || |||||||||| |||| |||| ||||||||
Db     301 ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTGTTGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Db     361 GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC 420

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[illegible]

QY	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCTACCACCTACCAGGGCAGTCTATGTTCGAGG	1320
QY	1366	CAGGATGGGGCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG	1380
QY	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
QY	1486	CGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAATACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
QY	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
QY	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATACCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
QY	1666	CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTGAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCCTAGCTGGCTGTGAGACCCTGCTGAGTCCAGTCGTTAGC	1680
QY	1726	TGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
QY	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
QY	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
QY	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCGCTTTGCCCTGGTAGGAGAGGCC	1920
QY	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGTCTCCCGTGGCCTGTACG	1980
QY	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
QY	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC	2100
QY	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205

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Db      2101  TTTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG 2160
Qy      2206  AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGC 2265
Db      2161  AAGAGCAAGCTACTTGTCTAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC 2220
Qy      2266  CAGCGGTACTTGCCTGACCTTCACCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG 2325
Db      2221  CAGCAGTATCTGCACTGACCTTCACCTGGAGCGCATCAACGCCAGCACCAGCGACCTG 2280
Qy      2326  GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC 2385
Db      2281  GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGGAGATGGGCAGAGCTTCAACATCAACTTC 2340
Qy      2386  AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTTC 2445
Db      2341  AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTTC 2400
Qy      2446  CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT 2505
Db      2401  CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAGATCATC 2460
Qy      2506  TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC 2565
Db      2461  GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAACTT 2520
Qy      2566  CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC 2625
Db      2521  CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC 2580
Qy      2626  AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
Db      2581  AACCTATGGGAGGCACGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640
Qy      2686  GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGAGGC 2745
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Qy      2746  CGGCCAG 2752
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RESULT 2

US-09-306-902A-1

; Sequence 1, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

```

;
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 268 BUSH STREET, SUITE 3200
;   CITY: SAN FRANCISCO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94104
;
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/306,902A
;   FILING DATE: 07-May-1999
;   CLASSIFICATION: <Unknown>
;
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OSMAN, RICHARD A
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: UC96-217
;
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 343-4341
;   TELEFAX: (415) 343-4342
;
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1

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Query Match          82.1%;  Score 2259;  DB 3;  Length 3014;
Best Local Similarity 89.7%;  Pred. No. 0;
Matches 2427;  Conservative 0;  Mismatches 280;  Indels 0;  Gaps 0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
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Db      1  ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT 60

Qy     106 CGCGGCTCGGGTGCCCGAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
        || || ||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CGTGGTTTCGGGTGCCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
        |||||||| |||||||||||||| |||| |||| |||||| ||||||||||
Db     121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
        ||| || | |||||||| |||| |||| |||||||||||||| ||||
Db     181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
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Db     241 TGGGTCCGCCAGGTGCATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGGAAGGTGTTGGGCTGGAG 405

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Db	361		420
		GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	
QY	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421		480
		TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	
QY	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCCGAG	585
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		TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	
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		GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCAATGTGTACATC	
QY	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACCTACACC	705
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		ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACCTACACC	
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		TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTGATTGTTTAT	
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Db	721		780
		GTGAACGGTGGGTGGTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	
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Db	781		840
		GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	
QY	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841		900
		TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	
QY	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901		960
		TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	
QY	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961		1020
		GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGCTGACCTGGAC	
QY	1066	ACCCGCAACTGTACCAAGTACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021		1080
		ACCCGCAACTGTACCAAGTACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	
QY	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGTGCTCCTCATC	1185
Db	1081		1140
		CTCTACATCGGCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	
QY	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245

Db	1141	CTCATTTACTGTGCGAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCTAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCGAGACCTCAGCACCACCCTACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAATACTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTACCGAGCAGCTGGGCCGCTTTGCCCTGGTGAGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040

Qy 2086 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC 2145  
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 Db 2041 GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCTGCAC 2100  
 Qy 2146 TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG 2205  
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 Db 2101 TTCAAGGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCCAGCTCCCTGTGG 2160  
 Qy 2206 AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACG 2265  
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 Db 2161 AAGAGCAAGCTACTTGTCTAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC 2220  
 Qy 2266 CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG 2325  
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 Db 2221 CAGCAGTATCTGCACTGCACCTTCACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG 2280  
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 Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC 2340  
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 Db 2401 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAAGATCATC 2460  
 Qy 2506 TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTC 2565  
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 Db 2461 GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAAACTT 2520  
 Qy 2566 CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC 2625  
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 Db 2521 CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC 2580  
 Qy 2626 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685  
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 Db 2581 AACCTATGGGAGGCACGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640  
 Qy 2686 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGAGGC 2745  
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 Db 2641 GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTGCGGAGGCCGAGTGTTGAGAC 2700  
 Qy 2746 CGGCCAG 2752  
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 Db 2701 CAGCCAG 2707

RESULT 3

US-08-808-982-2

; Sequence 2, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David



```

; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-2

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Query Match          56.8%; Score 1562.4; DB 2; Length 1787;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1661; Conservative 0; Mismatches 16; Indels 9; Gaps 8;

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Qy      1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249
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Qy      1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
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Qy	1309	ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG	1368
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Qy	1369	GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	1428
Db	300	GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	359
Qy	1429	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	1488
Db	360	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	419
Qy	1489	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	1548
Db	420	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	479
Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
Db	480	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC	539
Qy	1609	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAGCCG	1668
Db	540	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAGCCG	599
Qy	1669	GAAGACGTGAGGTTGCCCCCTAGCTGGCTGTGAGACCCTGCTGAGTCCCATCGTTAGCTGT	1728
Db	600	GAAGACGTGAGGTTGCCCCCTAGCTGGCTGTGAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCTGGCGTCTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	GGACCCCTGGCGTCTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTT-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG	2208

Db	1077	AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCAGCTCCCTGTGGAAG	1134
Qy	2209	AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	2268
Db	1135	AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	1254
Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
Db	1375	GCCCTGGTGGGCCCCAGTGCCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568
Db	1435	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	1494
Qy	2569	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	2628
Db	1495	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	1554
Qy	2629	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	2688
Db	1555	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	1614
Qy	2689	GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC	2746
Db	1615	GGGACTGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTTCGGAGGCTGAGTGCTGAGGCC	1674
Qy	2747	GGCCAG 2752	
Db	1675	GGCCAG 1680	

RESULT 4

US-09-306-902A-2

; Sequence 2, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

```

;
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 268 BUSH STREET, SUITE 3200
;   CITY: SAN FRANCISCO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94104
;
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/306,902A
;   FILING DATE: 07-May-1999
;   CLASSIFICATION: <Unknown>
;
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OSMAN, RICHARD A
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: UC96-217
;
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 343-4341
;   TELEFAX: (415) 343-4342
;
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1787 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-306-902A-2

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Query Match          56.8%;   Score 1562.4;   DB 3;   Length 1787;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 1661;   Conservative 0;   Mismatches 16;   Indels 169;   Gaps 8;

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Qy      1070 GCAACTGTACCAAGTACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACCTGGCCCTCT 1129
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Db      1 GCAACTGTACCAAGTACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACCTGGCCCTCT 59
          |||
Qy      1130 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCCTCG 1189
          |||
Db      60 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCCTCG 119
          |||
Qy      1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249
          |||
Db      120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179
          |||
Qy      1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
          |||
Db      180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 239
          |||
Qy      1309 ATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 1368
          |||
Db      240 ATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 299
          |||
Qy      1369 GATGGGCCCAGCCCCAAGTTCCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 1428
          |||

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Db	300	 GATGGGCCCAGCCCCAAGTTCCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	359
Qy	1429	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	1488
Db	360	 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	419
Qy	1489	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	1548
Db	420	 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	479
Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
Db	480	 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC	539
Qy	1609	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	1668
Db	540	 CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	599
Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	1728
Db	600	 GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCTGGCGTCCTGCTCACCCGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	 GGACCCCTGGCGTCCTGCTCACCCGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	 CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	 GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTT-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAG	2208
Db	1077	 AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCAGCTCCCTGTGGAAG	1134
Qy	2209	AGTAAGCTCCTTGTGCTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	2268

Db	1135	AGTAAGCTCCTTGTCTAGCTACCAAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCC	1254
Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	ATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTC	2508
Db	1375	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568
Db	1435	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	1494
Qy	2569	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	2628
Db	1495	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	1554
Qy	2629	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	2688
Db	1555	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	1614
Qy	2689	GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC	2746
Db	1615	GGGACTGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTTCGGAGGCTGAGTGCTGAGGCC	1674
Qy	2747	GGCCAG	2752
Db	1675	GGCCAG	1680

# RESULT 5

US-09-833-381-1806

; Sequence 1806, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1806

; LENGTH: 1282

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1282)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1806

Query Match 42.0%; Score 1155.8; DB 4; Length 1282;  
Best Local Similarity 98.2%; Pred. No. 3e-240;  
Matches 1263; Conservative 0; Mismatches 13; Indels 10; Gaps 9;

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Qy      1469 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 1528
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Db        1 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 60

Qy      1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588
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Db        61 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 120

Qy      1589 CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCT 1648
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Db       121 CAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCT 180

Qy      1649 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGC 1708
          |||
Db       181 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGC 240

Qy      1709 TGAGTCCCATCGTTAGCTGTGGACCCCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT- 1766
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Db       241 TGAGTCCCATCGTTAGCTGTGGACCCCTGGGCGTCCTGCTCACCCGGCCAGTCATCCTG 300

Qy      1767 GGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGC 1825
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Db       301 GGGTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGC 360

Qy      1826 AGTCGTGCGAGGGCAGCTGGGAGGATGTGC-TGCACCTGGGCGAGGAGGCGCCCTCCCAC 1884
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Db       361 AGTCGTGCGAGGGCAGCTGGGAGGATGTGCTTGCACCTGGGCGAGGAGGCGCCCTCCCAC 420

Qy      1885 CTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGC 1944
          |||
Db       421 CTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGC 480

Qy      1945 TTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG 2004
          |
Db       481 TATGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG 540

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Db       541 TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGAC 600

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          ||
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Qy      2125 CAGGAGCCACGGGTCTTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC 2184
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Qy	2185	GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCCTTT	2244
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Qy	2245	TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC	2304
Db	781	TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC	840
Qy	2305	AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG	2364
Db	841	AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG	900
Qy	2365	CAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCT	2424
Db	901	CAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCT	960
Qy	2425	CTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC	2484
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Qy	2485	CTCATTCGGCAGAAGATAA-TTTCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG	2543
Db	1021	CTCATTCGGCAGAAGATAATTTTCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG	1080
Qy	2544	GCGG-ACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC	2602
Db	1081	GCGGAACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC	1140
Qy	2603	CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC	2662
Db	1141	CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC	1200
Qy	2663	TCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAG	2722
Db	1201	TCAGCCAGCTGG-TGCAGCAGTGGCTGGACTGGGC--AGCAGACGCTGG-CTCTTCACAG	1256
Qy	2723	TGTCGGAGGCTGAGTGCTGAGGCCGG	2748
Db	1257	TGTCGGAGGCTGAGTGCTGAGGCCGG	1282

RESULT 6

US-08-808-982-3

; Sequence 3, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200



```

; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-3

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Query Match          30.6%; Score 841.4; DB 2; Length 2831;
Best Local Similarity 60.0%; Pred. No. 2.4e-172;
Matches 1638; Conservative 0; Mismatches 961; Indels 130; Gaps 9;

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Db      104 ACTCCTTCCCATCAGCACCCGCGGAGCAGCTGCCTCACTTCCTGCTGGAACCAAGAGGATG 163

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
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Db      164 CCTACATCGTAAAGAACAAGCCAGTGGAATTGCACTGCCGAGCCTTCCCTGCCACACAGA 223

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
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Db      224 TCTACTTCAAGTGTAATGGCGAGTGGGTTAGCCAGAAAGGCCACGTACGCAGGAGAGCC 283

Qy      323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
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Db      284 TGGATGAGGCCACAGGCTTGCGAATACGAGAGGTGCAGATAGAGGTGTGCGGGCAGCAGG 343

Qy      383 TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
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Db      344 TGGAGGAACCTTTTGGGCTCGAGGACTACTGGTGTCAGTGCGTGGCCTGGAGCTCCTCGG 403

Qy      443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      404 GAACCACCAAGAGTCGCCGAGCCTACATCCGCATTGCCTACTTGCAGCAAGAACTTTGACC 463

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Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
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 Db 464 AGGAGCCTCTGGCGAAGGAGGTACCCTTGGATCATGAGGTCCTTCTGCAGTGCCGCCCCAC 523

Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
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 Db 524 CAGAGGGAGTGCCTGTGGCTGAGGTGGAATGGCTCAAGAATGAAGATGTCATCGATCCCCG 583

Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGGACAGGCCCGCC 682  
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 Db 584 CTCAGGACACTAACTTCCTGCTCACCATTGACCACAACCTCATCATCCGCCAGGCGCGCC 643

Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGACGCG 742  
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 Db 644 TCTCAGACACAGCCAACTACACCTGTGTGGCAAAGAATATTGTGGCCAAGCGCCGGAGCA 703

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 Db 704 CGACGGCCACAGTCATCGTCTATGTGAACGGAGGTTGGTCCAGCTGGGCAGAATGGTCAC 763

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 764 CCTGCTCTAACCCTGCGGCCGAGGTTGGCAGAAACGTACTAGGACCTGCACCAACCCAG 823

Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCGAATGTCCAGAAAACAGCCTGCGCCA 922  
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 Db 824 CCCCCTCAATGGAGGTGCCTTCTGCGAGGGACAGGCTTGCCAGAAGACGGCTTGACCA 883

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCTGTGGGCTGG 982  
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 Db 884 CCGTGTGCCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCCGCCTGCAGCACAG 943

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
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 Db 944 AGTGTGCGCACTGGCGCAGCCGCGAGTGCATGGCACC GCCCGCCCGAGAACGGAGGCCGTG 1003

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
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 Db 1004 ACTGCAGCGGGACGCTACTTGACTCCAAGAACTGCACCGATGGGCTGTGCGTGCTGAATC 1063

Qy 1103 CTTCTGGCC-----CTGAGGACGTGGCCCTCT 1129  
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 Db 1064 AGAGAACTCTAAACGACCCTAAAAGCCGCCCCCTGGAGCCGTGCGGAGACGTGGCGCTGT 1123

Qy 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGCTGCTTGTCTCATCC 1186  
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 Db 1124 ATGCGGGCCTCGTGGTGGCCGTCTTGTGGTCTGTCAGTTCTCATGGCTGTAGGAGTGA 1183

Qy 1187 TCGTTTATTGCCGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C 1243  
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Qy 1244 TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGC 1303  
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Qy 1304 T-----CACCATCCAGCCGACCTCAGCACCACCACCACCCTACCAGGGCAGTCTCT 1357

Db 1304 TGCACCCATCCGCCCCTCCGGACCTAACGGCCAGTGCTGGCATCTACCGCGGACCTGTGT 1363  
 Qy 1358 GTCCCCGGCAGGA-----TG 1372  
 Db 1364 ATGCCCTGCAGGACTCTGCCGACAAGATCCCTATGACTAATTCACCCCTTCTGGATCCCT 1423  
 Qy 1373 GGCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCC-----CCTGG 1423  
 Db 1424 TGCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACCATCGGCTCTGGGGCTGGCCTGG 1483  
 Qy 1424 GTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCT 1483  
 Db 1484 CTGATGGAGCCGACCTGCTGGGTGTCTTACCACCCGGTACATACCCAGGCGATTTCTCCC 1543  
 Qy 1484 CCCGCCTCTCCACCCAGAAC-----TACTTCCGCTCCC 1516  
 Db 1544 GGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCCTTGGTTCACGACCTCCTGGGCC 1603  
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 Db 1604 TCCCTCGAGACCCCAGCAGCAGTGTGAGTGGCACCTTTGGTTGCCTGGGTGGGAGGCTGA 1663  
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 Db 1664 CCATTCCCGGCACAGGGGTGAGCCTGTTGGTACCAAATGGAGCCATTCCCCAGGGCAAGT 1723  
 Qy 1637 TCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTGCCCCCTAGCTGGCT 1696  
 Db 1724 TCTATGACTTGTATCTACGTATCAACAAGACTGAAAGCACCTCCCCTTTTCGGAAGGTT 1783  
 Qy 1697 GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCTGCTCACCCGGC 1756  
 Db 1784 CCCAGACAGTATTGAGCCCCTCGGTGACCTGCGGGCCACGGGCCTCCTCCTGTGCCGCC 1843  
 Qy 1757 CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCC 1816  
 Db 1844 CTGTTGTCCTCACTGTGCCCCACTGTGCTGAAGTCATTGCCGAGACTGGATCTTCCAGC 1903  
 Qy 1817 TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC 1876  
 Db 1904 TCAAGACCCAGGCCCCTCAGGGCCACTGGGAGGAGGTGGTGACTTTGGATGAGGAGACTC 1963  
 Qy 1877 CCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTACCGAGCAGC 1936  
 Db 1964 TGAACACCCCCTGCTACTGCCAGCTAGAGGCTAAATCCTGCCACATCCTGTTGGACCAGC 2023  
 Qy 1937 TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC 1996  
 Db 2024 TGGGTACCTACGTGTTACGGGCGAGTCCTACTCCCCTCCGAGTCAAGCGGCTCCAGC 2083  
 Qy 1997 TGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCC 2056  
 Db 2084 TAGCCATCTTCGCCCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTC 2143  
 Qy 2057 TGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAC 2116



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; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3

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Query Match          30.6%; Score 841.4; DB 3; Length 2831;
Best Local Similarity 60.0%; Pred. No. 2.4e-172;
Matches 1638; Conservative 0; Mismatches 961; Indels 130; Gaps 9;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
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Db      104 ACTCCTTCCCATCAGCACCCGCGGAGCAGCTGCCTCACTTCCTGCTGGAACCAGAGGATG 163

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      164 CCTACATCGTAAAGAACAAGCCAGTGGAATTGCACTGCCGAGCCTTCCCTGCCACACAGA 223

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      224 TCTACTTCAAGTGTAATGGCGAGTGGGTTAGCCAGAAAGGCCACGTACGCAGGAGAGCC 283

Qy      323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
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Db      284 TGGATGAGGCCACAGGCTTGCGAATACGAGAGGTGCAGATAGAGGTGTGCGGGCAGCAGG 343

Qy      383 TCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
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Db 344 TGGAGGAACTTTTTGGGCTCGAGGACTACTGGTGTCACTGCGTGGCCTGGAGCTCTTCGG 403  
 Qy 443 GCACCACCAAGAGTCAGAAGGCCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
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 Db 404 GAACCACCAAGAGTCGCCGAGCCTACATCCGCATTGCCTACTTGC GCAAGAACTTTGACC 463  
 Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 464 AGGAGCCTCTGGCGAAGGAGGTACCCCTGGATCATGAGGTCCCTTCTGCAGTGCCGCCCAC 523  
 Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
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 Db 524 CAGAGGGAGTGCCGTGGCTGAGGTGGAATGGCTCAAGAATGAAGATGTCATCGATCCCG 583  
 Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC 682  
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 Db 584 CTCAGGACACTAACTTCCTGCTCACCATTGACCACAACCTCATCATCCGCCAGGCGCGCC 643  
 Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCGAGCG 742  
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 Db 644 TCTCAGACACAGCCAACTACACCTGTGTGGCAAAGAATATTGTGGCCAAGCGCCGGAGCA 703  
 Qy 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 704 CGACGGCCACAGTCATCGTCTATGTGAACGGAGGTTGGTCCAGCTGGGCAGAATGGTCAC 763  
 Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 764 CCTGCTCTAACCCTGCGGCCGAGGTTGGCAGAAACGTACTAGGACCTGCACCAACCCAG 823  
 Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
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 Db 824 CCCCCTCAATGGAGGTGCCTTCTGCGAGGGACAGGCTTGCCAGAAGACGGCTTGACCA 883  
 Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCCGCTGTGGGCTGG 982  
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 Db 884 CCGTGTGCCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCCGCTGCAGCACAG 943  
 Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
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 Db 944 AGTGTGCGCACTGGCGCAGCCGCGAGTGCATGGCACC GCCCGCCCAAGACGGAGGCCGTG 1003  
 Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
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 Db 1004 ACTGCAGCGGGACGCTACTTGACTCCAAGAACTGCACCGATGGGCTGTGCGTGCTGAATC 1063  
 Qy 1103 CTTCTGGCC-----CTGAGGACGTGGCCCTCT 1129  
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 Db 1064 AGAGAACTCTAAACGACCCTAAAAGCCGCCCCCTGGAGCCGTGCGGAGACGTGGCGCTGT 1123  
 Qy 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCC 1186  
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 Db 1124 ATGCGGGCCTCGTGGTGGCCGTCTTTGTGGTTCTGGCAGTTCTCATGGCTGTAGGAGTGA 1183  
 Qy 1187 TCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C 1243  
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 Db 1184 TCGTGTACCGGAGAACTGCCGGGACTTCGACACGGACATCACTGACTCCTCTGCTGCCC 1243

Qy 1244 TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGC 1303  
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 Db 1244 TCACTGGTGGTTTCCACCCCGTCAACTTCAAGACTGCAAGGCCAGCAACCACAGCTCC 1303

Qy 1304 T-----CACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCT 1357  
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 Db 1304 TGCACCCATCCGCCCTCCGGACCTAACGGCCAGTGCTGGCATCTACCGCGGACCTGTGT 1363

Qy 1358 GTCCCCGGCAGGA-----TG 1372  
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 Db 1364 ATGCCCTGCAGGACTCTGCCGACAAGATCCCTATGACTAATTCACCCCTTCTGGATCCCT 1423

Qy 1373 GGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCC-----CCTGG 1423  
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 Db 1424 TGCCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACCATCGGCTCTGGGGCTGGCCTGG 1483

Qy 1424 GTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCT 1483  
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 Db 1484 CTGATGGAGCCGACCTGCTGGGTGTCTTACCACCCGGTACATACCCAGGCGATTCTCCC 1543

Qy 1484 CCCGCCTCTCCACCCAGAAC-----TACTTCCGCTCCC 1516  
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 Db 1544 GGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCCTTGGTTCCCAGCACCTCCTGGGCC 1603

Qy 1517 TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA 1576  
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 Db 1604 TCCCTCGAGACCCAGCAGCAGTGTGAGTGGCACCTTGGTTGCCTGGGTGGGAGGCTGA 1663

Qy 1577 TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGA 1636  
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 Db 1664 CCATTCCCGGCACAGGGGTGAGCCTGTTGGTACCAAATGGAGCCATTCCCCAGGGCAAGT 1723

Qy 1637 TCTATGAGATCTACCTCAGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCT 1696  
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 Db 1724 TCTATGACTTGTATCTACGTATCAACAAGACTGAAAGCACCCCTCCCCTTTTCGGAAGGTT 1783

Qy 1697 GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACCCGGC 1756  
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 Db 1784 CCCAGACAGTATTGAGCCCTCGGTGACCTGCGGGCCACGGGCCTCCTCCTGTGCCGCC 1843

Qy 1757 CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCC 1816  
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 Db 1844 CTGTTGTCCTCACTGTGCCCCACTGTGCTGAAGTCATTGCCGGAGACTGGATCTTCCAGC 1903

Qy 1817 TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC 1876  
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 Db 1904 TCAAGACCCAGGCCCATCAGGGCCACTGGGAGGAGGTGGTGACTTTGGATGAGGAGACTC 1963

Qy 1877 CCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCCTGCTACGTCTTCACCGAGCAGC 1936  
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 Db 1964 TGAACACCCCTGCTACTGCCAGCTAGAGGCTAAATCCTGCCACATCCTGTTGGACCAGC 2023

Qy 1937 TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC 1996  
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 Db 2024 TGGGTACCTACGTGTTACGGGCGAGTCCTACTCCCGCTCCGCAGTCAAGCGGCTCCAGC 2083





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; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1807
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1605)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1807
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Query Match          15.7%; Score 432; DB 4; Length 1605;
Best Local Similarity 62.5%; Pred. No. 4e-84;
Matches 737; Conservative 0; Mismatches 435; Indels 7; Gaps 4;
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Qy      1515 CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCT 1574
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Db      421 CCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCT 480

Qy      1575 GATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAA 1634
          | |||||
Db      481 CANCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCAATGGAGCCATTCCCCAGGGCAA 540

Qy      1635 GATCTATGA--GATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCCTAGCT 1692
          | |||||
Db      541 GTTCTACGAAGATGTATTCTACTCATCAACAAGGCAGAAAGTACCCTCCCGCTTTCAGAA 600

Qy      1693 GGCTGTGACACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACC 1752
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Db      601 GGGACCCANACAGTATTGAGCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGC 660

Qy      1753 CGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTG 1812
          || |||||
Db      661 CGCCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTT 720

Qy      1813 CGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAG 1872
          | |||||
Db      721 CAGCTCAAGACCCAGGCCCCACCAGGGCCACTGGGANGAGGTGGTGACCCTGGATGAGGAG 780

Qy      1873 GCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAG 1932
          | | |||||
Db      781 ACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTCACATCCTGCTGGAC 840

Qy      1933 CAGCTGGGCGCGCT-TTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCT 1991
          |||||
Db      841 CAGCTGGGCACCTACCGTGTTACGGGCGAGTCTATTCCCGCTCAGCAGTCAAGCGGCT 900

Qy      1992 CAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTA 2051
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Db	901	CCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTA	960
Qy	2052	CTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGG	2111
Db	961	CTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGG	1020
Qy	2112	GGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTACCACAACCTGCG	2171
Db	1021	CGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACCACAACCTGCG	1080
Qy	2172	CCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCA	2231
Db	1081	CCTCTCCCTCCATGACCTCCCCCATGCCCATTGGAGGAGCAAGCTGCTGGCCAAATACCA	1140
Qy	2232	GGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAGTGCACCTTCAC	2291
Db	1141	GGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCACCTTCAC	1200
Qy	2292	CCTGGAGCGTGTGAGCCCCAG-CACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGG	2350
Db	1201	CCTGGAGAGGCACAGGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAG	1260
Qy	2351	TGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG---GACACAAGGT	2407
Db	1261	TGGAAGGGGAGGGCCAGATATTCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCT	1320
Qy	2408	TTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGCCCCAGTG	2467
Db	1321	CCCTGGACACTCTCTGCTCTGCCCCTGGCAGCACTGTCACCACCCAGCTGGGACCTTATG	1380
Qy	2468	CCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTA	2527
Db	1381	CCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACAGCCTAGATGCCCCCAACT	1440
Qy	2528	GGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCT	2587
Db	1441	CACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCTGAATT	1500
Qy	2588	TCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACT	2647
Db	1501	ACTTTGCCACCAAAGCGAGCCCCACGGNTGTGATCCTGGACCTCTGGGAAGCTCTGCAGC	1560
Qy	2648	TCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGG	2686
Db	1561	AGGACGATGGGGACCTCAACAGCCTGNCGAGTGCCTTGG	1599

RESULT 9

US-08-253-155A-17/c

; Sequence 17, Application US/08253155A

; Patent No. 5691147

; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jeno

; APPLICANT: Draetta, Giulio

; TITLE OF INVENTION: CDK4 Binding Proteins

; NUMBER OF SEQUENCES: 95

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  LAHIVE & COCKFIELD
;   STREET:  60 State Street
;   CITY:  Boston
;   STATE:  MA
;   COUNTRY:  USA
;   ZIP:  02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  ASCII(text)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/253,155A
;   FILING DATE:  02-JUN-1994
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Vincent, Matthew P.
;   REGISTRATION NUMBER:  36,709
;   REFERENCE/DOCKET NUMBER:  MII-028
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617) 227-7400
;   TELEFAX:  (617) 227-5941
;   INFORMATION FOR SEQ ID NO:  17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  771 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
US-08-253-155A-17

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Query Match          9.8%;  Score 269;  DB 1;  Length 771;
Best Local Similarity 67.6%;  Pred. No. 4.6e-49;
Matches 406;  Conservative 1;  Mismatches 191;  Indels 3;  Gaps 2;

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Qy      1700 AGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAG 1759
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Db      738 AGACAGTATTGAGCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCCG 679

Qy      1760 TCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCA 1819
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Db      678 TCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCA 619

Qy      1820 AAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCT 1879
          || ||| | |||| | ||||| ||| || |||| | |||| | |
Db      618 AGACCCAGGCCACCCAGGGCCACTGGGAGGAGGTGGTGACCCTGGATGAGGAGACCCTGA 559

Qy      1880 CCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGG 1939
          | | || ||||| ||||| |||| |||| || || | |||||
Db      558 ACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTACATCCTGCTGGACCAGCTGG 499

Qy      1940 GCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGC 1999
          || || | ||| ||| || | || | ||| :|| ||||
Db      498 GCACCTACGTGTTACGGGCGAGTCCTATTCCCGCTCAGCAGTCAAGCGGSTCCAGCTGG 439

Qy      2000 TTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGC 2059

```

Db	438	CCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGACTCCGGGTCTACTGTCTGG	379
QY	2060	ATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGC	2119
Db	378	AGGACAGGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACT	319
QY	2120	TGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCA	2179
Db	318	TGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTAACACAACCTGCG-CTCTTCC	260
QY	2180	TCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCC	2239
Db	259	TCCATGACCTCCCCCATGCCCATTGGAGGAGCAAGCTGCTGGCCAAATACCAGGAGATCC	200
QY	2240	CCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGC	2299
Db	199	CCTTCTATCACATTTGGAGTGGAGCCAGAAGG--CCTCCACTGCACTTTTACCCTGGAGA	142
QY	2300	G 2300	
Db	141	G 141	

; TELEPHONE: (415) 343-4341  
 ; TELEFAX: (415) 343-4342  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 305 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-08-808-982-4

Query Match 4.3%; Score 119; DB 2; Length 305;  
 Best Local Similarity 68.1%; Pred. No. 7.8e-17;  
 Matches 209; Conservative 0; Mismatches 95; Indels 3; Gaps 3;

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Qy      1862 TGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACG 1921
          ||| ||||| | | | | | ||||| ||||| ||| ||| |||
Db      1   TGGATGAGGAGACCCCTGAACACACCCTGCTACTG-CAGCTGGAGCCCAGGGCCTG-TACA 58

Qy      1922 TCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCG 1981
          || | || ||||| || | | | || ||| || | | || |
Db      59   TCCTGCTGGACCAGCTGGGCACCTACGTTTTTCACGGGCGAGTCCTATTCCTCGCTCAGCAG 118

Qy      1982 CCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACA 2041
          ||||| ||| |||| | || || || | ||||| ||||| |||
Db      119  TCAAGCGGCTCCAGCTGGCCGT-TTCGCCCCGCCCTCTGCACCTCCCTGGAGTACAGCC 177

Qy      2042 TCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGA 2101
          ||||| ||||| ||||| | |||| | | |||| ||||| || |||||
Db      178  TCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGC 237

Qy      2102 AGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACC 2161
          | |||| ||| | || | ||||| || ||||| |||||
Db      238  GGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACC 297

Qy      2162 ACAACCT 2168
          |||||
Db      298  ACAACCT 304
  
```

# RESULT 11

US-09-306-902A-4

; Sequence 4, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

```

;          COUNTRY: USA
;          ZIP: 94104
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/306,902A
;          FILING DATE: 07-May-1999
;          CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: OSMAN, RICHARD A
;          REGISTRATION NUMBER: 36,627
;          REFERENCE/DOCKET NUMBER: UC96-217
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;    INFORMATION FOR SEQ ID NO: 4:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 305 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-306-902A-4

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Query Match          4.3%; Score 119; DB 3; Length 305;
Best Local Similarity 68.1%; Pred. No. 7.8e-17;
Matches 209; Conservative 0; Mismatches 95; Indels 3; Gaps 3;

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Qy      1862 TGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACG 1921
        ||| ||||| | | | | | ||||| ||||| ||| ||| |||
Db      1 TGGATGAGGAGACCCTGAACACACCCTGCTACTG-CAGCTGGAGCCCAGGGCCTG-TACA 58

Qy      1922 TCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCG 1981
        || | || ||||| || | | | || ||| | | | | | |||
Db      59 TCCTGCTGGACCAGCTGGGCACCTACGTTTTTCACGGGCGAGTCCTATTCCTCGCTCAGCAG 118

Qy      1982 CCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACA 2041
        ||||| ||| |||| | || || || | ||||| ||||| |||
Db      119 TCAAGCGGCTCCAGCTGGCCGT-TTCGCCCCGCCCTCTGCACCTCCCTGGAGTACAGCC 177

Qy      2042 TCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGA 2101
        ||||| ||||| ||||| || |||| | | |||| ||||| || |||||
Db      178 TCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGC 237

Qy      2102 AGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACC 2161
        | |||| ||| | || | ||||| || ||||| |||||
Db      238 GGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACC 297

Qy      2162 ACAACCT 2168
        |||||
Db      298 ACAACCT 304

```

```

RESULT 12
US-08-985-526-2
; Sequence 2, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
;   APPLICANT: Mixson, James A
;   TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
;   TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN
GENE
;   TITLE OF INVENTION: THERAPY
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Connolly, Bove, Lodge, & Hutz
;     STREET: 1220 Market Street, P.O. Box 2207
;     CITY: Wilmington
;     STATE: Delaware
;     COUNTRY: U.S.A.
;     ZIP: 19899
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/985,526
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/608,845
;     FILING DATE: 16-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McMorow Jr., Robert G
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (302) 658-9141
;     TELEFAX: (302) 658-5613
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 657 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-08-985-526-2

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Query Match          1.9%; Score 53.6; DB 3; Length 657;
Best Local Similarity 52.7%; Pred. No. 0.012;
Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

```

```

Qy      756 CATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAG 815
        || || || | | || | || | | || | || | || | || | || | || | ||
Db      222 CAGCGACTCTGCGGACGATGGCTGGTCTCCATGGTCCGAGTGGACCTCCTGTTCTACGAG 281

Qy      816 CTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGG 875
        || || || || || || || || || || || || || || || || || || || ||
Db      282 CTGTGGCAATGGAATTCAGCAGCGCGCCGCTCCTGCGATAGCCTCAACAACCGATGTGA 341

Qy      876 GGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGT 935
        || || | | || | || | || | || | || | || | || | || | || | ||

```

```

Db          342 GGGCTCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATTTAAACA 401
Qy          936 AGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGT 975
              || || ||||| ||| | ||||| |||
Db          402 GGATGGTGGCTGGAGCCACTGGTCCCCGTGGTCATCTTGT 441

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RESULT 13

US-08-985-526-4

; Sequence 4, Application US/08985526

; Patent No. 6080728

; GENERAL INFORMATION:

; APPLICANT: Mixson, James A

; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA

; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN

GENE

; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz

; STREET: 1220 Market Street, P.O. Box 2207

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: U.S.A.

; ZIP: 19899

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/608,845

; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorrow Jr., Robert G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-9141

; TELEFAX: (302) 658-5613

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1326 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-985-526-4

Query Match 1.9%; Score 53.6; DB 3; Length 1326;

Best Local Similarity 52.7%; Pred. No. 0.015;

Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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Qy          756 CATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAG 815
              || || || | | ||| ||| |||| | ||| ||||| || ||| | ||
Db          222 CAGCGACTCTGCGGACGATGGCTGGTCTCCATGGTCCGAGTGGACCTCCTGTTCTACGAG 281

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Qy      816 CTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGG 875
      |||||  ||  |||  ||  |||  |||  ||  ||  ||  ||
Db      282 CTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCGATAGCCTCAACAACCGATGTGA 341

Qy      876 GGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGT 935
      ||||  ||  ||  ||  |||  ||  ||  ||  ||  ||  ||
Db      342 GGGCTCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATTAAACA 401

Qy      936 AGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGT 975
      ||  ||  |||||  |||  ||  |||||  ||  |||
Db      402 GGATGGTGGCTGGAGCCACTGGTCCCCGTGGTCATCTTGT 441

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# RESULT 14

US-09-252-991A-7947

; Sequence 7947, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7947

; LENGTH: 699

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7947

Query Match 1.9%; Score 52.8; DB 4; Length 699;

Best Local Similarity 47.6%; Pred. No. 0.019;

Matches 156; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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Qy      1824 GCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCA 1883
      ||  ||  |||  ||  ||  ||  ||  ||  |||  ||  ||  ||  ||  ||  ||
Db      160 GCCGAAGTACGACGTCTACGACAGCAACGAGGTGCTCGAGGCCAAGCTGCTGTCCGGGCA 219

Qy      1884 CCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCG 1943
      |  ||||  ||  |||  |||  |||  ||  |||  ||  ||  ||  ||  ||  ||
Db      220 TTCCGGCTACGACCTGGTGGTGCCAGCGACAGCTTCCTGCCCCAACTACCTGAAGGCCGA 279

Qy      1944 CTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCT 2003
      |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  |||  ||  ||  ||
Db      280 GGTGTTCCAGCCGCTGGACAAGAGCAAGCTGCCGAAGTGAAGAACCTCAACCCGGCCCT 339

Qy      2004 GTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGA 2063
      |  |  |  |  |||  |||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      340 GCTCAAGGTGCTCGCCGGCAAGGACCCCGGCAACCGCTACGTGATGCCCTACATGTGGGG 399

```

```

Qy      2064 CACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGAT 2123
          ||| ||| | | | | | | | | | | | | | | | |
Db      400 CACCAACGGCATCGCCTACAACCTCGACAAGGTCCGCGCGGTGCTCGGCGACGATGCGCC 459

Qy      2124 CCAGGAGCCACGGGTCCTGCACTTCAAG 2151
          | ||| | ||| ||| | ||||
Db      460 GCTGGACTCCTGGGACCTGGTGTTCAG 487

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RESULT 15

US-09-252-991A-7809

; Sequence 7809, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7809

; LENGTH: 1302

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7809

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Query Match          1.9%; Score 52.8; DB 4; Length 1302;
Best Local Similarity 47.6%; Pred. No. 0.022;
Matches 156; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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Qy      1824 GCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCA 1883
          || | || ||| | | | | | | | | | | | | | | |
Db      360 GCCGAAGTACGACGTCTACGACAGCAACGAGGTGCTCGAGGCCAAGCTGCTGTCCGGGCA 419

Qy      1884 CCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCG 1943
          | ||| | | | | | | | | | | | | | | | |
Db      420 TTCCGGCTACGACCTGGTGGTGCCAGCGACAGCTTCCTGCCCAACTACCTGAAGGCCGA 479

Qy      1944 CTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCT 2003
          | || | | | | | | | | | | | | | | |
Db      480 GGTGTTCCAGCCGCTGGACAAGAGCAAGCTGCCGAAGTGAAGAACCTCAACCCGGCCCT 539

Qy      2004 GTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGA 2063
          | | | | | ||| || | || | | | | | | | |
Db      540 GCTCAAGGTGCTCGCCGGCAAGGACCCCGGCAACCGCTACGTGATGCCCTACATGTGGGG 599

Qy      2064 CACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGAT 2123
          ||| ||| | | | | | | | | | | | | | |
Db      600 CACCAACGGCATCGCCTACAACCTCGACAAGGTCCGCGCGGTGCTCGGCGACGATGCGCC 659

Qy      2124 CCAGGAGCCACGGGTCCTGCACTTCAAG 2151

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Db                    | | | | | | | | | |  
660 GCTGGACTCCTGGGACCTGGTGTTCAG 687

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Job time : 199 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2004, 18:05:13 ; Search time 1173 Seconds  
(without alignments)  
11434.720 Million cell updates/sec

Title: US-10-624-932-1  
Perfect score: 2752  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result                      %  
Query

No.	Score	Match	Length	DB	ID	Description
1	2752	100.0	2752	13	US-09-918-779-1	Sequence 1, Appli
2	2752	100.0	2752	17	US-10-624-932-1	Sequence 1, Appli
3	2676.4	97.3	2881	11	US-09-970-944-1	Sequence 1, Appli
4	2356	85.6	3580	17	US-10-311-623-13	Sequence 13, Appl
5	2259	82.1	3014	10	US-09-933-261-1	Sequence 1, Appli
6	2259	82.1	3014	15	US-10-256-702-1	Sequence 1, Appli
7	2252.2	81.8	2697	15	US-10-240-154-15	Sequence 15, Appl
8	1562.4	56.8	1787	10	US-09-933-261-2	Sequence 2, Appli
9	1562.4	56.8	1787	15	US-10-256-702-2	Sequence 2, Appli
10	1206.6	43.8	1321	13	US-10-296-115-365	Sequence 365, App
11	1155.8	42.0	1282	9	US-09-833-381-1806	Sequence 1806, Ap
12	936.2	34.0	2860	13	US-10-087-684-1	Sequence 1, Appli
13	936.2	34.0	2860	13	US-10-087-684-3	Sequence 3, Appli
14	936.2	34.0	2860	13	US-10-218-779-1	Sequence 1, Appli
15	936.2	34.0	2860	13	US-10-218-779-3	Sequence 3, Appli
16	913.6	33.2	2895	13	US-10-037-417-37	Sequence 37, Appl
17	904	32.8	3485	9	US-09-816-828-18	Sequence 18, Appl
18	902.4	32.8	3884	13	US-10-147-493-145	Sequence 145, App
19	902.4	32.8	3884	13	US-10-145-127-145	Sequence 145, App
20	902.4	32.8	3884	13	US-10-160-503-145	Sequence 145, App
21	902.4	32.8	3884	13	US-10-143-118-145	Sequence 145, App
22	902.4	32.8	3884	13	US-10-144-993-145	Sequence 145, App
23	902.4	32.8	3884	13	US-10-158-787-145	Sequence 145, App
24	902.4	32.8	3884	13	US-10-140-024-145	Sequence 145, App
25	902.4	32.8	3884	13	US-10-140-808-145	Sequence 145, App
26	902.4	32.8	3884	13	US-10-152-405-145	Sequence 145, App
27	902.4	32.8	3884	13	US-10-127-852A-145	Sequence 145, App
28	902.4	32.8	3884	13	US-10-127-900A-145	Sequence 145, App
29	902.4	32.8	3884	13	US-10-128-685A-145	Sequence 145, App
30	902.4	32.8	3884	13	US-10-131-820A-145	Sequence 145, App
31	902.4	32.8	3884	13	US-10-142-886-145	Sequence 145, App
32	902.4	32.8	3884	13	US-10-146-728-145	Sequence 145, App
33	902.4	32.8	3884	13	US-10-146-786-145	Sequence 145, App
34	902.4	32.8	3884	13	US-10-147-499-145	Sequence 145, App
35	902.4	32.8	3884	13	US-10-157-798-145	Sequence 145, App
36	902.4	32.8	3884	15	US-10-028-072-145	Sequence 145, App
37	902.4	32.8	3884	15	US-10-121-049-145	Sequence 145, App
38	902.4	32.8	3884	15	US-10-123-904-145	Sequence 145, App
39	902.4	32.8	3884	15	US-10-140-470-145	Sequence 145, App
40	902.4	32.8	3884	15	US-10-175-746-145	Sequence 145, App
41	902.4	32.8	3884	15	US-10-176-918-145	Sequence 145, App
42	902.4	32.8	3884	15	US-10-176-921-145	Sequence 145, App
43	902.4	32.8	3884	15	US-10-137-865-145	Sequence 145, App
44	902.4	32.8	3884	15	US-10-140-474-145	Sequence 145, App
45	902.4	32.8	3884	15	US-10-142-431-145	Sequence 145, App

#### ALIGNMENTS

RESULT 1  
 US-09-918-779-1  
 ; Sequence 1, Application US/09918779  
 ; Publication No. US20030064369A1  
 ; GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Spaderna, Steven  
 ; APPLICANT: Shimkets, Richard  
 ; APPLICANT: Zerhusen, Bryan  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Shenoy, Suresh  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gusev, Vladimir  
 ; APPLICANT: Grosse, William  
 ; APPLICANT: Alsobrook, John  
 ; APPLICANT: Lepley, Denise  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: MacDougall, John  
 ; APPLICANT: Stone, David  
 ; APPLICANT: Smithson, Glennnda  
 ; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-074 US  
 ; CURRENT APPLICATION NUMBER: US/09/918,779  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/221,409  
 ; PRIOR FILING DATE: 2000-07-28  
 ; PRIOR APPLICATION NUMBER: 60/222,840  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,752  
 ; PRIOR FILING DATE: 2000-08-08  
 ; PRIOR APPLICATION NUMBER: 60/223,762  
 ; PRIOR FILING DATE: 2000-08-08  
 ; PRIOR APPLICATION NUMBER: 60/223,770  
 ; PRIOR FILING DATE: 2000-08-08  
 ; PRIOR APPLICATION NUMBER: 60/223,769  
 ; PRIOR FILING DATE: 2000-08-08  
 ; PRIOR APPLICATION NUMBER: 60/225,146  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/225,392  
 ; PRIOR FILING DATE: 2000-08-15  
 ; PRIOR APPLICATION NUMBER: 60/225,470  
 ; PRIOR FILING DATE: 2000-08-15  
 ; PRIOR APPLICATION NUMBER: 60/225,697  
 ; PRIOR FILING DATE: 2000-08-16  
 ; PRIOR APPLICATION NUMBER: 60/263,662  
 ; PRIOR FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: 60/281,645  
 ; PRIOR FILING DATE: 2001-04-05  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2752  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-918-779-1

Query Match 100.0%; Score 2752; DB 13; Length 2752;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCGGGGCCCCGCGCCCGGCCCCGCCCGCTGCCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
      |||
Db      1 CCGCGGGGCCCCGCGCCCGGCCCCGCCCGCTGCCCCGCCCGCGGCCATGGCCGTCCGGCCC 60

Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
      |||
Db     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120

Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
      |||
Db    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

Qy    181 TTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db    181 TTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
      |||
Db    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC 360
      |||
Db    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC 360

Qy    361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db    361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420

Qy    421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db    421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
      |||
Db    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540

Qy    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
      |||
Db    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600

Qy    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
      |||
Db    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660

Qy    661 CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
      |||
Db    661 CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720

Qy    721 ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGG 780
      |||
Db    721 ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGG 780

Qy    781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
      |||
Db    781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Db	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Qy	1021	GCACCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	GCACCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGCCGG	1200
Db	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Qy	1321	CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1321	CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Db	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Db	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Qy	1501	AATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Db	1501	AATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680



Qy	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Db	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Db	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Db	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Qy	1861	CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Db	1861	CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Qy	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Db	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Db	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Qy	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGACAGTTAC	2160
Db	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGACAGTTAC	2160
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCGAGCGGTACTTGCAC	2280
Db	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCGAGCGGTACTTGCAC	2280
Qy	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Db	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Qy	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Db	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Qy	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Db	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Qy	2461	CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Db	2461	CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Qy	2521	CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580

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Db      2521  |||||
                CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT 2580

Qy      2581  CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
                |||||

Db      2581  CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
                |||||

Qy      2641  CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
                |||||

Db      2641  CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
                |||||

Qy      2701  CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
                |||||

Db      2701  CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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## RESULT 2

US-10-624-932-1

```

; Sequence 1, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769

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; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1
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Query Match          100.0%; Score 2752; DB 17; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 CCGCGGGGCCCCGCGCCCGGCCCCGCCGCTGCCCGCCGCGGCCATGGCCGTCCGGCCC 60

Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
      |||
Db     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120

Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
      |||
Db    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

Qy    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy    241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
      |||
Db    241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
      |||
Db    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360

Qy    361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db    361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420

Qy    421 TGCGTGGCATGGAGCTCCTCGGGCACCAACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db    421 TGCGTGGCATGGAGCTCCTCGGGCACCAACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
      |||
Db    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540

Qy    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Db	541	 ATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Qy	601	AACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Db	601	 AACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Qy	661	CTGGTGGTGCGACAGGCCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	661	 CTGGTGGTGCGACAGGCCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Qy	721	ATCGTGGCACGTGCGCCGACGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Db	721	 ATCGTGGCACGTGCGCCGACGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	781	 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	841	 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Db	961	 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Qy	1021	GCACCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	 GCACCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Db	1141	 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1261	 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Qy	1321	CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1321	 CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGGCCGCACACA	1440

Db	1381	CCCAAGTTCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Db	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Qy	1501	AAC TACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Db	1501	AAC TACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Qy	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGC	1740
Db	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Db	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Db	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Qy	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Db	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Qy	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Db	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Db	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Qy	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC	2160
Db	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC	2160
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Db	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280

Qy	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Db	2281	TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Qy	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Db	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Qy	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Db	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Qy	2461	CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Db	2461	CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Qy	2521	CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580
Db	2521	CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580
Qy	2581	CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Db	2581	CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Qy	2641	CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
Db	2641	CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
Qy	2701	CCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGAGGCCGGCCAG	2752
Db	2701	CCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGAGGCCGGCCAG	2752

# RESULT 3

US-09-970-944-1

; Sequence 1, Application US/09970944

; Publication No. US20030204052A1

## ; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2881

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-970-944-1

Query Match 97.3%; Score 2676.4; DB 11; Length 2881;  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

Qy	1	CCGCGGGGGCCCCGCGCCCGGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCCC	60
Db	42	CCGCGGGGGCCCCGCGCCCGGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCCC	101
Qy	61	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	120
Db	102	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	161
Qy	121	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	180
Db	162	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC	221
Qy	181	TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	240
Db	222	TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	281
Qy	241	AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	300
Db	282	AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	341
Qy	301	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC	360
Db	342	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC	401
Qy	361	ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG	420
Db	402	ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG	461
Qy	421	TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC	480
Db	462	TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC	521
Qy	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Db	522	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	581
Qy	541	ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Db	582	ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	641
Qy	601	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Db	642	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	701
Qy	661	CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	702	CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	761
Qy	721	ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG	780
Db	762	ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG	821

Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	822	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCAGAAAT	900
Db	882	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCAGAAAT	941
Qy	901	GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCCTGG	957
Db	942	GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCCTGG	1001
Qy	958	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1017
Db	1002	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1061
Qy	1018	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1077
Db	1062	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1121
Qy	1078	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1137
Db	1122	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1181
Qy	1138	CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGC	1197
Db	1182	CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGC	1241
Qy	1198	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1257
Db	1242	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1301
Qy	1258	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGCTCACCATCCAGCCG	1317
Db	1302	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGCTCACCATCCAGCCG	1361
Qy	1318	GACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1377
Db	1362	GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1418
Qy	1378	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1437
Db	1419	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1478
Qy	1438	AACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1497
Db	1479	AACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1557
Db	1539	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1598
Qy	1558	TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1617
Db	1599	TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1658
Qy	1618	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1677



Db	1659	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1718
Qy	1678	AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT	1737
Db	1719	AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT	1778
Qy	1738	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1797
Db	1779	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1914
Db	1899	CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1958
Qy	1915	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2034
Db	2019	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2078
Qy	2035	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2094
Db	2079	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTCAAGGAC	2154
Db	2139	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTCAAGGAC	2198
Qy	2155	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2274
Db	2259	CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2334
Db	2319	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2378
Qy	2335	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2394
Db	2379	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2438
Qy	2395	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2454
Db	2439	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2498
Qy	2455	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2514

Db 2499 GTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2558  
 Qy 2515 GACCCACCCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC 2574  
 Db 2559 GACCCACCCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC 2618  
 Qy 2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634  
 Db 2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678  
 Qy 2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694  
 Db 2679 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2738  
 Qy 2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752  
 Db 2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2796

#### RESULT 4

US-10-311-623-13

; Sequence 13, Application US/10311623

; Publication No. US20040023244A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.

; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.

; APPLICANT: YUE, Henry; NGUYEN, Danniel B.

; APPLICANT: TANG, Y. Tom; LAL, Preeti G.

; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda

; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.

; APPLICANT: YAO, Monique G.; BURFORD, Neil

; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.

; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.

; APPLICANT: YANG, Junming; XU, Yuming

; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.

; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.

; APPLICANT: DUGGAN, Brendan M.; LU, Yan

; TITLE OF INVENTION: RECEPTORS

; FILE REFERENCE: PF-0793 USN

; CURRENT APPLICATION NUMBER: US/10/311,623

; CURRENT FILING DATE: 2002-12-17

; PRIOR APPLICATION NUMBER: US 01/19942

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: US 60/214,027

; PRIOR FILING DATE: 2000-06-21

; PRIOR APPLICATION NUMBER: US 60/228,045

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/255,104

; PRIOR FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PERL Program

; SEQ ID NO 13

; LENGTH: 3580

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1  
US-10-311-623-13

Query Match 85.6%; Score 2356; DB 17; Length 3580;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

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Qy      43 GCCATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG 102
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Db       1 GCCATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG 60

Qy     103 CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 162
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 120

Qy     163 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 222
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 180

Qy     223 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 282
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 240

Qy     283 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 342
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 300

Qy     343 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAAGGTGTTTCGGGCTG 402
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAAGGTGTTTCGGGCTG 360

Qy     403 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 462
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 420

Qy     463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 522
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     421 GCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 480

Qy     523 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC 582
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC 540

Qy     583 GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 642
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 600

Qy     643 ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC 702
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC 660

Qy     703 ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTC 762
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTC 720

Qy     763 TACGTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGG 822
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Db 721 TACGTG----- 726  
 QY 823 CGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCT 882  
 Db 727 ----- 726  
 QY 883 TTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGC 942  
 Db 727 -----GACGGC 732  
 QY 943 AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC 1002  
 Db 733 AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC 792  
 QY 1003 CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGGCACTGACCTG 1062  
 Db 793 CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGGCACTGACCTG 852  
 QY 1063 GACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG 1122  
 Db 853 GACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG 912  
 QY 1123 GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTC 1182  
 Db 913 GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTC 972  
 QY 1183 ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1242  
 Db 973 ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1032  
 QY 1243 CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG 1302  
 Db 1033 CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG 1092  
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 Db 1093 CTCACCATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCC 1152  
 QY 1363 CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG 1422  
 Db 1153 CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG 1212  
 QY 1423 GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC 1482  
 Db 1213 GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC 1272  
 QY 1483 TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGCACCAGCAACATGACC 1542  
 Db 1273 TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGCACCAGCAACATGACC 1332  
 QY 1543 TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC 1602  
 Db 1333 TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTC 1392  
 QY 1603 CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC 1662  
 Db 1393 CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC 1452

Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1782
Db	1513	AGCTGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1572
Qy	1783	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1842
Db	1573	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1632
Qy	1843	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1902
Db	1633	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1692
Qy	1903	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1962
Db	1693	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1752
Qy	1963	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	2022
Db	1753	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	2142
Db	1873	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	1932
Qy	2143	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	2202
Db	1933	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2052
Qy	2263	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2322
Db	2053	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2112
Qy	2323	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2382
Db	2113	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2172
Qy	2383	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2232
Qy	2443	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2502
Db	2233	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2292

Qy 2503 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2562  
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 Db 2293 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2352  
 Qy 2563 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2622  
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 Db 2353 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2412  
 Qy 2623 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682  
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 Db 2413 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2472  
 Qy 2683 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742  
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 Db 2473 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2532  
 Qy 2743 GGCCGGCCAG 2752  
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 Db 2533 GGCCGGCCAG 2542

RESULT 5

US-09-933-261-1

; Sequence 1, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

```

;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 3014 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

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Query Match          82.1%;  Score 2259;  DB 10;  Length 3014;
Best Local Similarity 89.7%;  Pred. No. 0;
Matches 2427;  Conservative 0;  Mismatches 280;  Indels 0;  Gaps 0;

Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
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Db      1  ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCCTGGCTT 60

Qy     106 CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCG 165
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Db      61 CGTGGTTCGGGTGCCAGCAGAGTGCCACCGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
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Db     121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
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Db     181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
      |||| |||||||| || |||| || |||||| || || |||| || ||||
Db     241 TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTGGAG 405
      |||||||||||||| || || || || |||||||||| |||| |||| ||||||
Db     301 ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTCGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Db     361 GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAGTCAGAAGGCC 420

Qy     466 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 525
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Db     421 TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG 480

Qy     526 TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG 585
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Db     481 TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG 540

Qy     586 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 645
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Db     541 GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC 600

Qy     646 ACGCGGGAGCACAGCCTGGTGGTGGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC 705

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Db	601	 ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC	765
Db	661	 TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	 GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	 TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	 GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	 ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC	1185
Db	1081	 CTCTACATCGGCCTTGTTCGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	 CTCATTTACTGTCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	 ACCTCGGGCTTCCAGCCTGTTCAGCATCAAGCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	 ACCATCCAGCCAGACCTCAGCACCACCACCTACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	 CAGGATGGACCCAGCCCCAAGTTCAGCTCTCTAATGGTCACCTGCTCAGCCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	 AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545



Db	1441	CGCCTCTCCACCCAAACTACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTGCTGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGCAAGCTACTTGTGCTGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCCTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCCTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGGACGGGCAGAGCTTACAGCATCAACTTC	2385
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;          CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/09/933,261
;          FILING DATE: 20-Aug-2001
;          APPLICATION NUMBER: 08/808,982
;          FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;          NAME: OSMAN, RICHARD A
;          REGISTRATION NUMBER: 36,627
;          REFERENCE/DOCKET NUMBER: UC96-217
;
; TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 3014 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;
;          MOLECULE TYPE: cDNA
;
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1

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Query Match          82.1%;   Score 2259;   DB 15;   Length 3014;
Best Local Similarity 89.7%;   Pred. No. 0;
Matches 2427;   Conservative    0;   Mismatches 280;   Indels    0;   Gaps    0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGGCTC 105
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Db      1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT 60

Qy     106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
        || || ||||||||||||||||||||||| ||||||| ||||||| ||||||| |||
Db      61 CGTGGTTCGGGTGCCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
        ||||||| ||||||||||||||| ||||| ||||| ||||||| ||||||| |||
Db     121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
        ||| || | ||||||||||| ||||| ||||| ||||||| ||||||| |||||
Db     181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
        ||||| ||||||| || ||||| || || ||||||| ||| | ||||| || |||
Db     241 TGGGTCCGCCAGGTGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAGGTGTTCCGGGCTGGAG 405
        ||||||||||||| || || || || ||||||| ||||| ||||| |||||||
Db     301 ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTGTTGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Db     361 GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC 420

Qy     466 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 525
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Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGGCCACTGGCCAAGGAAGTG	480
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Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCA TTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGTCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGGCACTGACCTGGAC	1065
Db	961	GAGTGTCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTGAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCTACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320

Qy	1366	CAGGATGGGCCCCAGCCCCAAGTTCAGCTCACC	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCAGCTCTCTAATGGTCACCTGCTCAGCCCCCTGGGT	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAACACTACTTTCGTTCCCTGCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGAGAGGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGCCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160

Qy	2206	AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGCAAGCTACTTGTCTAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCCTGCACCTTCACCCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCCTGCACCTTCACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAAGATCATC	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAACTT	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625
Db	2521	CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC	2580
Qy	2626	AACCTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Db	2581	AACCTATGGGAGGCACGGCACCTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG	2640
Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGC	2745
Db	2641	GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTCTGGAGGCCGAGTGTTGAGAC	2700
Qy	2746	CGGCCAG 2752	
Db	2701	CAGCCAG 2707	

; TYPE: DNA  
; ORGANISM: Rattus sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2697)  
US-10-240-154-15

Query Match 81.8%; Score 2252.2; DB 15; Length 2697;  
Best Local Similarity 89.7%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
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Db       1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGTCTCCTGGGCATAGTCCTCGCCGCTTGGCTT 60

Qy     106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
      || ||
Db      61 CGTGGTTCGGGTGCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAGCCA 225
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Db     121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
      ||| ||
Db     181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
      ||| |||
Db     241 TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAG 405
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Db     301 ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTGTTGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Db     361 GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC 420

Qy     466 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 525
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Db     421 TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG 480

Qy     526 TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG 585
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Db     481 TCACTGGAGCAAGGCATTGTACTACCTTGTGCGCCCCCAGAAGGAATCCCCCAGCTGAG 540

Qy     586 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 645
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Db     541 GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC 600

Qy     646 ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTACACC 705
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Db     601 ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACCTACACC 660

Qy     706 TGCCTGGCCAAGAACATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTAC 765
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Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCTTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAAGTACCTCTGTGTACACAGTGTCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAAGTACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCTCATC	1185
Db	1081	CTCTACATCGGCCTTGTCTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCTAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACCTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAACCTACTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560



Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCGTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAGGACAGTTACCACAACCTACGTCTCTCCATCCACGAGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGCAAGCTACTTGTGAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTACCCTGGAGCGTGTGAGCCCGAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCACTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATACCAAGGACACAAGGTTTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400

Qy 2446 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT 2505  
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 Db 2401 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAAGATCATC 2460  
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 Db 2461 GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAAACTT 2520  
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 Db 2521 CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC 2580  
 Qy 2626 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685  
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 Db 2581 AACCTATGGGAGGCACGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640  
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 Db 2641 GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTGCGGAGGCCGAGTGTTGA 2697

RESULT 8

US-09-933-261-2

; Sequence 2, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

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;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 2:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 1787 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: double
;               TOPOLOGY: linear
;           MOLECULE TYPE: cDNA
;           SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2

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Query Match          56.8%;   Score 1562.4;   DB 10;   Length 1787;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 1661;   Conservative    0;   Mismatches    16;   Indels      9;   Gaps      8;

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Qy      1070 GCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCT 1129
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Db        1 GCAACTGTACCAGTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCT 59

Qy      1130 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTGTCTCATCCTCG 1189
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Db        60 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTGTCTCATCCTCG 119

Qy      1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249
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Db        120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179

Qy      1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
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Db        180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 239

Qy      1309 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 1368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 299

Qy      1369 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 359

Qy      1429 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 1488
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Db        360 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 419

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG 479

Qy      1549 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC 1608
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Db        480 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC 539

Qy      1609 CCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG 1668
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Db        540 CCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG 599

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Db	600	 GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCTGGCGTCCTGCTACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	 GGACCCCTGGCGTCCTGCTACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	 CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	 GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG	2208
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Qy	2209	AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	2268
Db	1135	 AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	1254
Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	 ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
Db	1375	 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568

Db 1435 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC 1494  
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 Db 1555 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 1614  
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 Db 1615 GGGACTGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTTCGGAGGCTGAGTGCTGAGGCC 1674  
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RESULT 9

US-10-256-702-2

; Sequence 2, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/256,702

; FILING DATE: 27-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

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;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 2:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 1787 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: double
;               TOPOLOGY: linear
;           MOLECULE TYPE: cDNA
;           SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-256-702-2

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Query Match          56.8%;   Score 1562.4;   DB 15;   Length 1787;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 1661;   Conservative    0;   Mismatches    16;   Indels      9;   Gaps      8;

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Qy      1070 GCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCT 1129
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Db            120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179

Qy      1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
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Db            180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 239

Qy      1309 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 1368
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Db            240 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 299

Qy      1369 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            300 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 359

Qy      1429 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            360 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 419

Qy      1489 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG 1548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            420 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG 479

Qy      1549 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            480 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC 539

Qy      1609 CCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            540 CCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG 599

Qy      1669 GAAGACGTGAGGTTGCCCTAGCTGGCTGTCTAGACCCCTGCTGAGTCCCATCGTTAGCTGT 1728

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Db	600	 GAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	 GGACCCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	 CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	 GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG	2208
Db	1077	 AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCCAGCTCCCTGTGGAAG	1134
Qy	2209	AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	2268
Db	1135	 AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	1254
Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	 ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
Db	1375	 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568

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Db      1435 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC 1494
Qy      2569 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1495 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 1554
Qy      2629 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1555 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 1614
Qy      2689 GGAAGTGGGCGAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC 2746
          ||      |||||||      |||      |||      ||      ||||||||      ||||||||||||
Db      1615 GGGACTGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTTCGGAGGCTGAGTGCTGAGGCC 1674
Qy      2747 GGCCAG 2752
          |||||||
Db      1675 GGCCAG 1680

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RESULT 10

US-10-296-115-365

; Sequence 365, Application US/10296115

; Publication No. US20040053248A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq Inc

; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 784PCT

; CURRENT APPLICATION NUMBER: US/10/296,115

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: US09/488,725

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US09/552,317

; PRIOR FILING DATE: 2000-04-25

; NUMBER OF SEQ ID NOS: 1478

; SEQ ID NO 365

; LENGTH: 1321

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-296-115-365

```

Query Match          43.8%;  Score 1206.6;  DB 13;  Length 1321;
Best Local Similarity 98.0%;  Pred. No. 1.6e-296;
Matches 1295;  Conservative 0;  Mismatches 19;  Indels 7;  Gaps 7;

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Qy      1435 CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC 1494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1    CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC 60
Qy      1495 ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC 1554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61   ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC 120
Qy      1555 AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCA 1614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCA 180
Qy      1615 GATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC 1674

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Db	181	 GATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC	240
Qy	1675	GTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	1734
Db	241	 GTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	300
Qy	1735	CCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-GGCTATGGACCACTGT-GGGGAGCCC	1791
Db	301	 CCTGGGCGTCCTGCTTACCCGGCCAGTCATCCTGGGGTATGGACCACTGTGGGGGAGCCC	360
Qy	1792	AGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	1850
Db	361	 AGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	420
Qy	1851	TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	1910
Db	421	 TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	480
Qy	1911	TGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAG	1970
Db	481	 TGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATGCCCTGGTGGGAGAGGCCCTCAG	540
Qy	1971	CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	2030
Db	541	 CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	600
Qy	2031	CGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGT	2090
Db	601	 CGAGTACAACATACTGGTCTACTGCCTGCATGACACTCACGATGCACTCAACGTAGTGGT	660
Qy	2091	GCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTCAA	2150
Db	661	 GCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGGAGCCACTGGTACTGCACCTCAA	720
Qy	2151	GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	2210
Db	721	 GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	780
Qy	2211	TAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCAGCG	2270
Db	781	 TAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCAGCG	840
Qy	2271	GTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	2330
Db	841	 GTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	900
Qy	2331	CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	2390
Db	901	 CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	960
Qy	2391	CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	2450
Db	961	 CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	1020
Qy	2451	CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG	2510

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Db      1021 CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG 1080
Qy      2511 CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT 2570
          |||
Db      1081 CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT 1140
Qy      2571 GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT 2630
          |||
Db      1141 GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT 1200
Qy      2631 GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT-G 2689
          |||
Db      1201 GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGG 1260
Qy      2690 GACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCCG 2747
          |||
Db      1261 GACTGGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTTCGGAGGCTGAGTGCTGAGGCCG 1320
Qy      2748 G 2748
          |
Db      1321 G 1321

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RESULT 11

US-09-833-381-1806

; Sequence 1806, Application US/09833381

; Patent No. US20020132090A1

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1806

; LENGTH: 1282

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(1282)

; OTHER INFORMATION: n = A,T,C or G

US-09-833-381-1806

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Query Match          42.0%;  Score 1155.8;  DB 9;  Length 1282;
Best Local Similarity 98.2%;  Pred. No. 1.3e-283;
Matches 1263;  Conservative 0;  Mismatches 13;  Indels 10;  Gaps 9;

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Qy      1469 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 1528
          |||
Db       1 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 60
Qy      1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588
          |||

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Db	61	CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA	120
Qy	1589	CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	1648
Db	121	CAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	180
Qy	1649	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	1708
Db	181	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	240
Qy	1709	TGAGTCCCATCGTTAGCTGTGGACCCCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-	1766
Db	241	TGAGTCCCATCGTTAGCTGTGGACCCCTGGGCGTCCTGCTCACCCGGCCAGTCATCCTG	300
Qy	1767	GGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGC	1825
Db	301	GGGTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGC	360
Qy	1826	AGTCGTGCGAGGGCAGCTGGGAGGATGTGC-TGCACCTGGGCGAGGAGGCGCCCTCCCAC	1884
Db	361	AGTCGTGCGAGGGCAGCTGGGAGGATGTGCTTGCACCTGGGCGAGGAGGCGCCCTCCCAC	420
Qy	1885	CTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGC	1944
Db	421	CTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGC	480
Qy	1945	TTTGGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG	2004
Db	481	TATGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG	540
Qy	2005	TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGAC	2064
Db	541	TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGAC	600
Qy	2065	ACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATC	2124
Db	601	ACTCACGATGCACTCAACGTAGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATC	660
Qy	2125	CAGGAGCCACGGGTCTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC	2184
Db	661	CAGGAGCCACGGGTCTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC	720
Qy	2185	GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTT	2244
Db	721	GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTT	780
Qy	2245	TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC	2304
Db	781	TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC	840
Qy	2305	AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG	2364
Db	841	AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG	900
Qy	2365	CAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCT	2424
Db	901	CAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCT	960

Qy	2425	CTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC	2484
Db	961	CTGGAGAGTGAAGCGNGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC	1020
Qy	2485	CTCATTCGGCAGAAGATAA-TTTCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG	2543
Db	1021	CTCATTCGGCAGAAGATAATTTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG	1080
Qy	2544	GCGG-ACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC	2602
Db	1081	GCGGAACCTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC	1140
Qy	2603	CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC	2662
Db	1141	CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC	1200
Qy	2663	TCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAG	2722
Db	1201	TCAGCCAGCTGG-TGCAGCAGTGGCTGGACTGGGC--AGCAGACGCTGG-CTCTTCACAG	1256
Qy	2723	TGTCGGAGGCTGAGTGCTGAGGCCGG	2748
Db	1257	TGTCGGAGGCTGAGTGCTGAGGCCGG	1282

RESULT 12

US-10-087-684-1

; Sequence 1, Application US/10087684

; Publication No. US20040029116A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: MacDougall, John R.

; APPLICANT: Millet, Isabelle

; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David J.

; APPLICANT: Grosse, William M.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Cathereine E.

; APPLICANT: Casman, Stacie, J.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Li, Li

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Mishra, Vishnu

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Rastelli, Luca

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Miller, Charles E.

; APPLICANT: Gangolli, Esha A.

; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-214 CIP

```

; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

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Query Match          34.0%; Score 936.2; DB 13; Length 2860;
Best Local Similarity 61.7%; Pred. No. 9.1e-228;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
      || | | || | | | | | | | | | | | | | | | | | | |
Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
      || || | | | | | | | | | | | | | | | | | | | |
Db      228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
      || | | | | | | | | | | | | | | | | | | | | | |
Db      288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy      323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
      || | | | | | | | | | | | | | | | | | | | | | |
Db      348 TGGATGAGGCCACCGGTCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

Qy      383 TCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
      | || | | | | | | | | | | | | | | | | | | | | |
Db      408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG 467

Qy      443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
      || || || || || || || || || || || || || || || ||
Db      468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy      503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562
      || || || | || | | | | | | | | | | | | | | | | |
Db      528 AGGAGCCTCTGGGCAAGGAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCCG 587

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Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 ||||| | ||| ||||| ||||| ||||| ||| ||||| | | |||||  
 Db 588 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647

Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGGACAGGCCCCGCC 682  
 ||| |||| |||| | |||| || |||| ||| | | |||||  
 Db 648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 707

Qy 683 TTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742  
 | | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 708 TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 767

Qy 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTGGACGTGGACCGAGTGGTCCG 802  
 || | || | ||||| ||||| || || ||||| | ||| | |||||  
 Db 768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGTGGTCCAGCTGGGCAGAGTGGTCAC 827

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 |||| | | ||||| || ||||| ||||| || ||||| ||||| ||||| |||||  
 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 887

Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | || ||||| || || ||||| ||||| ||| ||||| || ||||| |||||  
 Db 888 CTCCACTCAACGGAGGGGCCCTTCTGCGAGGGCCAGGCATTCAGAAAGACCGCCTGCACCA 947

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCTGTGGGCTGG 982  
 || | ||||| || || ||||| ||||| ||||| ||||| ||||| | |  
 Db 948 CCATCTGCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | || ||||| ||||| ||||| ||||| | || ||||| ||||| |||||  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | || | || || || ||||| ||||| || || || || || || || || ||  
 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127

Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | || || || || || || || || || || || || || || || || || || || ||  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGG 1187

Qy 1163 TCCTGCTGCTGCTTGTCTCATCTCGTTTATTGCCGGAAGAAGAGGGGGCTGGACTCAG 1222  
 | || | || || || || || || || || || || || || || || || || || ||  
 Db 1188 CAATCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247

Qy 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
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 Db 1248 ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307

Qy 1280 GCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
 | | | ||||| || || || || || || || || || || || || || || || ||  
 Db 1308 CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367

Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCGGCAGGA----- 1370  
 || || |||| | || | || || |||||  
 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427

Qy 1371 -----TGGGCCCAGCCCCAAGTTCAGCTCACCA----- 1399

Db	1428	CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA		1487
Qy	1400	--ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC		1447
Db	1488	CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG		1547
Qy	1448	ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACT		1507
Db	1548	GCACATACCCTAGCGATTTCGCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC		1607
Qy	1508	TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT		1552
Db	1608	TCGGTTCCTCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT		1667
Qy	1553	TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC		1612
Db	1668	TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA		1727
Qy	1613	CAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG		1672
Db	1728	ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA		1787
Qy	1673	ACGTGAGGTTGCCCCTAGCTGGCTGTGAGCCCTGCTGAGTCCCATCGTTAGCTGTGGAC		1732
Db	1788	GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC		1847
Qy	1733	CCCCTGCGCTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA		1792
Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCGTCATCCTCACCATGCCCACTGTGCCGAAGTCA		1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG		1852
Db	1908	GTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG		1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG		1912
Db	1968	TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG		2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG		1972
Db	2028	CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCCTATTCCC		2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG		2032
Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG		2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC		2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG		2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTTCAAGG		2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG		2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA		2212





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; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

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Query Match          34.0%; Score 936.2; DB 13; Length 2860;
Best Local Similarity 61.7%; Pred. No. 9.1e-228;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
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Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
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Db      228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTTCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
        || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy      323 CAGACGGGAGCAGTGGGCTGCCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
        || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      348 TGGATGAGGCCACCGGCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

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Qy 383 TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442  
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 Db 408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAG 467

Qy 443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
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 Db 468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 528 AGGAGCCTCTGGGCAAGGAGGTGCCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC 587

Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 588 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTATCGACCCCA 647

Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC 682  
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 Db 648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCGCCAGGCCCGCC 707

Qy 683 TTGCTGACACGGCCAATACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 708 TGTGCGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 767

Qy 743 CCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 768 CCACTGCCACCGTTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAAGCGCACCCGGACCTGCACCAACCCG 887

Qy 863 CGCCTCTCAACGGGGGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 888 CTCCACTCAACGGAGGGGCGCTTCTGCGAGGGCCAGGCATTCAGAAGACCGCCTGCACCA 947

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCTGTGGGCTGG 982  
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 Db 948 CCATCTGCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCCACCACAGAACGGAGGCCGTG 1067

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
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 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127

Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGG 1187

Qy 1163 TCCTGCTGCTGCTTGTCTCATCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG 1222  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247

Qy	1223	ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1248	ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTCCACCCCGTCAACTTTAAGACGG	1307
Qy	1280	GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA	1333
Db	1308	CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG	1367
Qy	1334	CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA-----	1370
Db	1368	CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA	1427
Qy	1371	-----TGGGCCAGCCCCAAGTTCCAGCTCACCA-----	1399
Db	1428	CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA	1487
Qy	1400	--ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC	1447
Db	1488	CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG	1547
Qy	1448	ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAATACT	1507
Db	1548	GCACATAACCCTAGCGATTTGCCCCGGGACACCCACTTCTGCACCTGCGCAGCGCCAGCC	1607
Qy	1508	TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT	1552
Db	1608	TCGGTTCACAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT	1667
Qy	1553	TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCC	1612
Db	1668	TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGTGGTGCCCA	1727
Qy	1613	CAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG	1672
Db	1728	ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA	1787
Qy	1673	ACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGAC	1732
Db	1788	GTACCCTGCCGCTTTTCTAGAGGGACCCAGACAGTATTGAGCCCCCTCGGTGACCTGTGGAC	1847
Qy	1733	CCCTGGCGCTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA	1792
Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCGCTCATCCTCACCATGCCCACTGTGCCGAAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG	1852
Db	1908	GTGCCCGTGACTGGATCTTTTCTAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG	2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCTATTCCC	2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032

Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC	2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACCTTCAAGG	2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268	ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCATGCCCATTTGGAGGAGCA	2327
Qy	2213	AGCTCCTTGTGCTAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCAGCAGCGGT	2272
Db	2328	AGCTGCTGGCCAAATACCAGGAGATCCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273	ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388	CCCTCCACTGCACTTTTACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA	2392
Db	2448	AGATCTGCGTGCGGCAAGTGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG	2507
Qy	2393	CCAAG---GACACAAGGTTTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAG	2449
Db	2508	CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCCTGGCAGCACTGTACCA	2567
Qy	2450	CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCA	2509
Db	2568	CCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACA	2627
Qy	2510	GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACC	2569
Db	2628	GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA	2687
Qy	2570	TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC	2629
Db	2688	TGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACC	2747
Qy	2630	TGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG	2689
Db	2748	TCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG	2807
Qy	2690	GACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGCTGA	2742
Db	2808	AGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA	2860

RESULT 14

US-10-218-779-1

; Sequence 1, Application US/10218779

; Publication No. US20040029222A1

; GENERAL INFORMATION:

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; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2860
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-218-779-1

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Query Match          34.0%; Score 936.2; DB 13; Length 2860;
Best Local Similarity 61.7%; Pred. No. 9.1e-228;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
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Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

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QY	203	TGTACATCGTCAAGAACAAAGCCAGTGTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA	262
Db	228	CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA	287
QY	263	TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA	322
Db	288	TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC	347
QY	323	CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG	382
Db	348	TGGATGAGGCCACCGGTCTGCGGGTGCGGAGGTGCAGATCGAGGTGTGCGGGCAGCAGG	407
QY	383	TCGAGAAGGTGTTGCGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG	442
Db	408	TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG	467
QY	443	GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC	502
Db	468	GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC	527
QY	503	AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC	562
Db	528	AGGAGCCTCTGGGCAAGGAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC	587
QY	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622
Db	588	CGGAGGGGGTGCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA	647
QY	623	CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC	682
Db	648	CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCGCCAGGCCCGCC	707
QY	683	TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG	742
Db	708	TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA	767
QY	743	CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCG	802
Db	768	CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC	827
QY	803	TCTGCAGCGCCAGCTGTGGGCGCGGTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG	862
Db	828	CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG	887
QY	863	CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA	922
Db	888	CTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA	947
QY	923	CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGG	982
Db	948	CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG	1007
QY	983	ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG	1042
Db	1008	AGTGTGCCCACTGGCGTAGCCGCGAGTGTCATGGCGCCCCCACCACAGAACGGAGGCCGTG	1067
QY	1043	AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG	1102

Db	1068	ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG	1127
Qy	1103	CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG	1162
Db	1128	AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGTGG	1187
Qy	1163	TCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG	1222
Db	1188	CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG	1247
Qy	1223	ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1248	ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG	1307
Qy	1280	GCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA	1333
Db	1308	CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG	1367
Qy	1334	CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA-----	1370
Db	1368	CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA	1427
Qy	1371	-----TGGGCCCAGCCCCAAGTTCAGCTCACCA-----	1399
Db	1428	CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA	1487
Qy	1400	--ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC	1447
Db	1488	CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG	1547
Qy	1448	ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCTGCTCTCCCGCCTCTCCACCCAGAATACT	1507
Db	1548	GCACATAACCTAGCGATTTGCCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC	1607
Qy	1508	TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT	1552
Db	1608	TCGGTTCCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT	1667
Qy	1553	TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCC	1612
Db	1668	TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA	1727
Qy	1613	CAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG	1672
Db	1728	ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA	1787
Qy	1673	ACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGAC	1732
Db	1788	GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC	1847
Qy	1733	CCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA	1792
Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG	1852

Db 1908 GTGCCCCGTGACTGGATCTTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG 1967  
 Qy 1853 TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG 1912  
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 Db 1968 TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG 2027  
 Qy 1913 CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG 1972  
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 Db 2028 CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCATTATCCC 2087  
 Qy 1973 TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG 2032  
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 Db 2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCGCCCCCTGTCACCTCCCTGG 2147  
 Qy 2033 AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC 2092  
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 Db 2148 AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCTGTAGCACTGAAGGAGGTGCTGG 2207  
 Qy 2093 AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGG 2152  
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 Db 2208 AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG 2267  
 Qy 2153 ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA 2212  
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 Db 2268 ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCATGCCCATTTGGAGGAGCA 2327  
 Qy 2213 AGCTCCTTGTCTAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGT 2272  
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 Db 2328 AGCTGCTGGCCAAATACCAGGAGATCCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG 2387  
 Qy 2273 ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCAGCACTAGTGACCTGGCCTGCA 2332  
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 Db 2388 CCCTCCACTGCACCTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA 2447  
 Qy 2333 AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA 2392  
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 Db 2448 AGATCTGCGTGCGGCAAGTGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG 2507  
 Qy 2393 CCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAG 2449  
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 Db 2508 CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCCTGGCAGCACTGTCACCA 2567  
 Qy 2450 CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCTCATTCGGCAGAAGATAATTTCCA 2509  
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 Db 2568 CCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACA 2627  
 Qy 2510 GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACC 2569  
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 Db 2628 GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA 2687  
 Qy 2570 TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC 2629  
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 Db 2688 TGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACC 2747  
 Qy 2630 TGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG 2689  
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 Db 2748 TCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG 2807



Qy 2690 GACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742  
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 Db 2808 AGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA 2860

RESULT 15

US-10-218-779-3

; Sequence 3, Application US/10218779  
 ; Publication No. US20040029222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: MacDougall, John  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Stone, David  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Grosse, William  
 ; APPLICANT: Alsobrook II, John  
 ; APPLICANT: Lepley, Denise  
 ; APPLICANT: Rieger, Daniel  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Casman, Stacie  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Shenoy, Suresh  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Tchernev, Velizar  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Zerhusen, Bryan  
 ; APPLICANT: Malyankar, Uriel  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Miller, Charles  
 ; APPLICANT: Gangolli, Esha  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-214  
 ; CURRENT APPLICATION NUMBER: US/10/218,779  
 ; CURRENT FILING DATE: 2002-08-14  
 ; PRIOR APPLICATION NUMBER: 60/253,834  
 ; PRIOR FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: 60/250,-926  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 60/264,180  
 ; PRIOR FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: 60/313,656  
 ; PRIOR FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: 60/327,456  
 ; PRIOR FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 216  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2860  
 ; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-218-779-3

Query Match 34.0%; Score 936.2; DB 13; Length 2860;  
Best Local Similarity 61.7%; Pred. No. 9.1e-228;  
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
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Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
      || || | | | | | | | | | | | | | | | | | | | |
Db      228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTTCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCCCCAGGTGGACCACGTGATCGAGCGCAGCA 322
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Db      288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy      323 CAGACGGGAGCAGTGGGCTGCCACCATTGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
      || | | | | | | | | | | | | | | | | | | | | | |
Db      348 TGGATGAGGCCACCGGCCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

Qy      383 TCGAGAAGGTGTTCCGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
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Db      408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAG 467

Qy      443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
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Db      468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy      503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562
      || || || || || || || || || || || || || || || ||
Db      528 AGGAGCCTCTGGGCAAGGAGGTGCCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC 587

Qy      563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622
      || || || | | || | | | | | | | | | | | | | | | |
Db      588 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647

Qy      623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC 682
      || | | | | | | | | | | | | | | | | | | | | | |
Db      648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 707

Qy      683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742
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Db      708 TGTGCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 767

Qy      743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCG 802
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Db      768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827

Qy      803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862
      || | | | | | | | | | | | | | | | | | | | | | |
Db      828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 887

Qy      863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922
      | | | | | | | | | | | | | | | | | | | | | | | |
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Db 888 CTCCACTCAACGGAGGGGCCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 947  
 Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGG 982  
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 Db 948 CCATCTGCCCACTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007  
 Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
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 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067  
 Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
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 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127  
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 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGCCATCTTCGTGGTCTGTGG 1187  
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 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247  
 Qy 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
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 Db 1248 ACATCACTGACTCATCTGTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307  
 Qy 1280 GCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
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 Db 1308 CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367  
 Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA----- 1370  
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 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427  
 Qy 1371 -----TGGGCCCAGCCCCAAGTTCCAGCTCACCA----- 1399  
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 Db 1428 CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487  
 Qy 1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447  
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 Db 1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547  
 Qy 1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACT 1507  
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 Db 1548 GCACATACCCTAGCGATTTGCCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607  
 Qy 1508 TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT 1552  
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 Db 1608 TCGGTTCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667  
 Qy 1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC 1612  
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 Db 1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA 1727  
 Qy 1613 CAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672  
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 Db 1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787

Qy	1673	ACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGAC	1732
Db	1788	GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCCTCGGTGACCTGTGGAC	1847
Qy	1733	CCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA	1792
Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG	1852
Db	1908	GTGCCCCTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGACCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG	2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCTATTCCC	2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032
Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC	2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGG	2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268	ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTTGGAGGAGCA	2327
Qy	2213	AGCTCCTTGTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCAGCGAGCGGT	2272
Db	2328	AGCTGCTGGCCAAATACCAGGAGATCCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273	ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388	CCCTCCACTGCACTTTTACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA	2392
Db	2448	AGATCTGCGTGCGGCAAGTGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG	2507
Qy	2393	CCAAG---GACACAAGGTTTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAG	2449
Db	2508	CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCCTGGCAGCACTGTACCA	2567
Qy	2450	CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCA	2509
Db	2568	CCCAGCTGGGACCTTATGCCTTCAAGATCCCCTGTCCATCCGCCAGAAGATATGCAACA	2627

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Qy      2510 GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACC 2569
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Db      2628 GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA 2687

Qy      2570 TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC 2629
          |||| | | | | | ||||| ||| | ||||| | ||||| |||
Db      2688 TGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACC 2747

Qy      2630 TGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG 2689
          | |||| | | | |||          | | | ||||| | ||||          | | | |
Db      2748 TCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG 2807

Qy      2690 GACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA 2742
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Db      2808 AGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA 2860

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Search completed: July 12, 2004, 22:55:54  
Job time : 1188 secs